

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2002, 19:19:10 ; Search time 61.73 Seconds

(without alignments)
759.325 Million cell updates/sec

Title: US-09-765-068-2

Perfect score: 2248

Sequence: 1 MDHPSREDEHQRTTKPMAO.....EAKCCFFKRRKKTQAKRK 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*

1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2248	100.0	422	22	AAG67392
2	2248	100.0	422	22	AAU04636
3	2219.5	98.7	459	22	AAG67542
4	2157	96.0	438	22	AA897904
5	1669.5	74.3	377	15	AAR56529
6	1669.5	74.3	377	16	AAR76625
7	1571.5	69.9	347	15	AAR56530
8	1571.5	69.9	347	16	AAR76626
9	1553	69.1	422	22	ABR66550
10	1553	69.1	422	22	ABR71525
11	942.5	41.9	416	21	AAV90264

12	938	41.7	476	21	AAG45046	Arabidopsis thalia
13	936	41.6	415	15	AAR56531	Protein kinase (CK
14	936	41.6	415	16	AAR76627	Human HRR25-like c
15	933	41.5	468	21	AA45810	Arabidopsis thalia
16	930	41.4	475	21	AA641798	Arabidopsis thalia
17	930	41.4	475	21	AA46931	Arabidopsis thalia
18	930	41.4	479	21	AA411797	Arabidopsis thalia
19	930	41.4	479	21	AA46930	Arabidopsis thalia
20	927	41.2	471	21	AA631488	Arabidopsis thalia
21	927	41.2	471	21	AA639489	Arabidopsis thalia
22	924	41.1	365	15	AAR56520	Protein kinase (Hh
23	924	41.1	365	16	AAR76616	Schizosaccharomyce
24	921	41.0	321	21	AA630651	Arabidopsis thalia
25	918.5	40.9	450	21	AA631130	Arabidopsis thalia
26	918	40.8	451	21	AA630687	Arabidopsis thalia
27	918	40.8	457	21	AA630686	Arabidopsis thalia
28	907.5	40.4	400	15	AAR56521	Protein kinase (Hh
29	907.5	40.4	400	16	AAR76617	Schizosaccharomyce
30	903.5	40.2	474	22	AAU00538	Maize casein kinas
31	900	39.9	475	21	AA639947	Arabidopsis thalia
32	897.5	39.9	433	21	AA609277	Arabidopsis thalia
33	897.5	39.9	433	21	AA643458	Arabidopsis thalia
34	890.5	39.6	435	21	AA639733	Arabidopsis thalia
35	885	39.4	440	22	AB858733	Drosophila melanog
36	885	39.4	440	22	AB867179	Drosophila melanog
37	885	39.4	440	22	AB867180	Wild-type Drosophi
38	884	39.3	440	21	AA601923	Mutant Drosophila
39	880	39.1	440	21	AA601925	Mutant Drosophila
40	876	39.0	440	21	AA601924	Protein kinase (CK
41	862.5	38.4	335	15	AAR56522	Human HRR25-like c
42	862.5	38.4	337	15	AAR76618	Protein kinase (CK
43	862.5	38.4	337	15	AAR56524	Human HRR25-like c
44	862.5	38.4	337	16	AAR76620	Human prostate can
45	862.5	38.4	332	21	AAR56608	

ALIGNMENTS

RESULT	1
AA67392	standard; Protein: 422 AA.
ID	AA67392
XX	AA67392:
AC	13-NOV-2001 (first entry)
XX	
DE	Amino acid sequence of human protein kinase SGK248.
KW	Human; protein kinase; cancer; immune disease; cardiovascular disease;
KW	brain disease; neuronal disease; Alzheimer's disease; chromosome 3;
KW	Parkinson's disease; multiple sclerosis; metabolic disorder;
KW	peripheral nervous system disease; amyotrophic lateral sclerosis;
KW	infection; ocular disease; migraine; pain; sexual dysfunction;
KW	mood disorder; attention disorder; cognition disorder; hypertension;
KW	hypertension; psychotic disorder; dyskinesia; transplant rejection.
XX	
OS	Homo sapiens.
XX	
PN	WO200166594-A2.
XX	
PD	13-SEP-2001.
XX	
PF	02-MAR-2001; 2001MO-US06838.
XX	
PR	06-MAR-2000; 2000US-0187150.
XX	
PR	29-MAR-2000; 2000US-0193404.
XX	
PR	13-NOV-2000; 2000US-0247013.
XX	
PA	(SUGEN) SUGEN INC.
XX	
PI	Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

DR WPI: 2001-536777/59.
DR N-PSDB: AAH77991.
XX
PT Nucleic acids capable of encoding human polypeptides having a kinase or
PT kinase-like activity, useful for diagnosing a disease selected from
PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT Alzheimer's disease) -
XX
PS Claim 7; Fig 2A; 201pp: English.
XX
XX The present sequence represents a human protein kinase. The
CC gene is located at chromosomal position 3p24.2-p21.3. The kinase
CC polypeptides are useful for diagnosing a disease or disorder
CC selected from cancers (e.g. cancers of tissues and cancers of
CC hematopoietic origin), immune-related diseases and disorders,
CC cardiovascular disease, brain or neuronal-associated diseases (e.g.
CC Alzheimer's disease, Parkinson's disease, multiple sclerosis),
CC metabolic disorders, peripheral nervous system diseases, amyotrophic
CC lateral sclerosis, viral infections, infections caused by prions,
CC infections caused by bacteria, infections caused by fungi, ocular
CC diseases, migraines, pain, sexual dysfunction, mood disorders,
CC attention disorders, cognition disorders, hypotension, hypertension,
CC psychotic disorders, dyskinesias, and organ transplant rejection.
CC Kinase inhibitors are useful for treating diseases and disorders
CC described above.
XX
SQ Sequence 422 AA:

Query Match 100.0%; Score 2248; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 5.7e-231;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHPSREDEQRRTTKPAQRSACSRPSGSSSGVLMVGNPNRVGKKICGNFGEI 60
DB 1 mdhpsrederqrrtkpmagrsahcsrpsgsassgvlmvgpnfrvgkkgcgnfgeir 60
QY 61 GKNLYTNEYVAIKLEPIKSRAPOLHLEFRFYKQLGSAGEGLPOYYFGPCGKYNAMVLEL 120
DB 61 gknlytneyvaiklepiksrappqlhleyrfykqlgsageglpvyvfygpcgkynamvlel 120
QY 121 LGSLEDFDLCDFRTFKTLVMTAIOQLSMREYVHSKNLIYRDVKPKNFLIGROGNKE 180
DB 121 lgsleedfdldcfrtftklvmtaioqlsmreyvhsknliyrdvknpenfligrgnke 180
QY 181 HVHIIDGLAKEVIDPEPKKHIPYREKSLTGARVYSINTHLGKEQSRDDLEALGHM 240
DB 181 hvhiidglakeyldpeckkhipreksltgcarvysinthlgkeqsrddlealghm 240
QY 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKRNTPIEALCENFPBEMATYLRVRRDLFFE 300
DB 241 fmyflrsglspwoglkadtlkerykigdtkrntpialcenfpemamatylrvrrldffe 300
QY 301 KPDVEYLRTLFTDLFEKKGYTFDYAVDWGRRPIPPVGSVHVDGASAITRESHTHRDRP 360
DB 301 kpdveylrtilftdlfekkytfdyavdwgrrpippvgsvhvdgsaaitreshthdrp 360
QY 361 SQOQPLRNQOVYSTNGELNVDDPTGAHSNAPITAAEVEVVEAKCCCFEKKRKKTAQR 420
DB 361 sqqplrnqvsvstngelnvddptgahsnapitahaeveveakcccfekrkrtktaqr 420
QY 421 HK 422
DB 421 hk 422

RESULT 2
ID AAU04636 standard; Protein: 422 AA.
XX
AC AAU04636;
XX
DT 26-SEP-2001 (first entry)

XX
DE Human kinase protein.
XX
KM Human: kinase protein; hybridisation probe; therapeutic; gene therapy;
XX antisense-therapy; drug screening.
XX
OS Homo sapiens.
XX
PN WO200153493-A2.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US02120.
XX
PR 18-JAN-2000; 2000US-0176690.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Donoho G, Hlibun E, Turner CA, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI: 2001-442260/47.
DR N-PSDB: AAS08535.
XX
XX An isolated nucleic acid molecule encoding a novel human protein useful
PT as therapeutics and to screen libraries isolate clones and prepare
PT cloning and sequencing templates -
XX
PS Claim 2; Page 31-32; 33pp: English.
XX
XX The sequence represents the amino acid sequence of a novel human kinase
CC protein. The nucleic acid sequence can be used to screen libraries,
CC isolate clones and prepare cloning and sequencing templates and as
CC hybridisation probes for screening libraries, and as therapeutics such
CC as antisense-therapy and gene-therapy. Probes derived from the DNA
CC or polypeptide sequences can be used in the identification, selection
CC and validation of novel molecular targets for drug discovery.
XX
SQ Sequence 422 AA:

Query Match 100.0%; Score 2248; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 5.7e-231;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHPSREDEQRRTTKPAQRSACSRPSGSSSGVLMVGNPNRVGKKICGNFGEI 60
DB 1 mdhpsrederqrrtkpmagrsahcsrpsgsassgvlmvgpnfrvgkkgcgnfgeir 60
QY 61 GKNLYTNEYVAIKLEPIKSRAPOLHLEFRFYKQLGSAGEGLPOYYFGPCGKYNAMVLEL 120
DB 61 gknlytneyvaiklepiksrappqlhleyrfykqlgsageglpvyvfygpcgkynamvlel 120
QY 121 LGSLEDFDLCDFRTFKTLVMTAIOQLSMREYVHSKNLIYRDVKPKNFLIGROGNKE 180
DB 121 lgsleedfdldcfrtftklvmtaioqlsmreyvhsknliyrdvknpenfligrgnke 180
QY 181 HVHIIDGLAKEVIDPEPKKHIPYREKSLTGARVYSINTHLGKEQSRDDLEALGHM 240
DB 181 hvhiidglakeyldpeckkhipreksltgcarvysinthlgkeqsrddlealghm 240
QY 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKRNTPIEALCENFPBEMATYLRVRRDLFFE 300
DB 241 fmyflrsglspwoglkadtlkerykigdtkrntpialcenfpemamatylrvrrldffe 300
QY 301 KPDVEYLRTLFTDLFEKKGYTFDYAVDWGRRPIPPVGSVHVDGASAITRESHTHRDRP 360
DB 301 kpdveylrtilftdlfekkytfdyavdwgrrpippvgsvhvdgsaaitreshthdrp 360
QY 361 SQOQPLRNQOVYSTNGELNVDDPTGAHSNAPITAAEVEVVEAKCCCFEKKRKKTAQR 420
DB 361 sqqplrnqvsvstngelnvddptgahsnapitahaeveveakcccfekrkrtktaqr 420

QY 421 HK 422
 II
 Db 421 hk 422

RESULT 3

AA67542 standard; Protein; 459 AA.

AA67542;

26-NOV-2001 (first entry)

Amino acid sequence of human kinase 15977.

Human; kinase; 2504; 15977; 14760; cellular proliferative disorder;
 cellular differentiative disorder; neural disorder; immune disorder;
 cardiovascular disorder; liver disorder; skin disorder;
 skeletal muscle disorder; bone metabolism; cardiovascular disorder;
 viral disease; pain; metabolic disorder; blood vessel disorder;
 hepatic disorder; liver disorder.

Homo sapiens.

Location/Qualifiers

14..16 /note- "predicted protein kinase C phosphorylation site"

44..329 /note- "serine/threonine kinase domain"

44..276 /note- "eukaryotic protein kinase domain"

96..99 /note- "predicted casein kinase II phosphorylation site"

124..127 /note- "predicted casein kinase II phosphorylation site"

137..139 /note- "predicted protein kinase C phosphorylation site"

150..153 /note- "predicted casein kinase II phosphorylation site"

199..201 /note- "predicted protein kinase C phosphorylation site"

214..216 /note- "predicted protein kinase C phosphorylation site"

229..231 /note- "predicted protein kinase C phosphorylation site"

229..232 /note- "predicted casein kinase II phosphorylation site"

258..260 /note- "predicted protein kinase C phosphorylation site"

258..261 /note- "predicted casein kinase II phosphorylation site"

269..271 /note- "predicted casein kinase II phosphorylation site"

270..273 /note- "predicted protein kinase C phosphorylation site"

273..276 /note- "predicted CAMP- and cAMP-dependent protein kinase phosphorylation site"

355..357 /note- "predicted casein kinase II phosphorylation site"

355..358 /note- "predicted protein kinase C phosphorylation site"

370..373 /note- "predicted casein kinase II phosphorylation site"

373..375 /note- "predicted N-glycosylation site"

388..391 /note- "predicted protein kinase C phosphorylation site"

411..414 /note- "predicted N-glycosylation site"

451..454 /note- "predicted casein kinase II phosphorylation site"

/note- "predicted CAMP- and cAMP-dependent protein kinase phosphorylation site"

Modified-site 422..427
 /note- "predicted N-myristoylation site"

Modified-site 46..49
 /note- "predicted amidation site"

WO200164905-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US06525.

29-FEB-2000; 2000US-0186061.

(MILL-) MILLENNIUM PHARM INC.

Olandt PJ, Kapeller-Libermann R, Meyers RA;
 WPI; 2001-570697/64.

New protein kinase family polypeptides for treating hematopoietic
 neoplastic disorders, immune disorders, cardiovascular disorders and
 disorders of blood vessels

Claim 8; Fig 4A-C; 145pp; English.

The present sequence represents human kinase 15977. The specification
 also describes kinases 2504 and 14760. The kinase polypeptides and
 polynucleotides are used to treat cellular proliferative or
 differentiative disorders, neural disorders, immune disorders,
 cardiovascular disorders, liver disorders, skin disorders and skeletal
 muscle disorders. They may also be used for controlling disorders
 associated with bone metabolism, cardiovascular disorders, viral
 diseases, pain or metabolic disorders, blood vessel
 disorders, and hepatic or liver disorders.

Sequence 459 AA:

Query Match 98.7%; Score 2219.5; DB 22; Length 459;

Best Local Similarity 91.9%; Pred. No. 7.2e-228; Matches 422; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

1 MDHPSREKDERQRTTKPMAQSAHCSRPSSSSSGVLMVGNFVGGKIKGNGELRL 60
 1 mdhpsrekderqrttkpmaqsahcsrpssssssgvlmvgnfvgkikgngelrll 60
 61 GKNLYTNEYVAIKLEPIKSAPOHLLEYRFYKQLGSAEGLPQVYIFGPGCKYAMVLEL 120
 61 gknllytneyvaiklepiksapohlleyrfykqlgsaeglpvyifpgpcgkyamvlel 120
 121 LGPSLEDLPFLCDRTFLKTVLMAIOLLSRMEVYHSKNLIYRKYRKNPFLIGRGNKKE 180
 121 lgpsledlpflcdrtflktvlmaiolllsrmevyhsknliyrkyrknnpfligrgnkke 180
 181 HVHIIDFGLAKEYIDDETKKHIPYREHKSITGVARVMSINTHLGKQSRDDEALGGM 240
 181 hvhiidfglakeyiddeatkhiipyrehksitgvarvmsinthlgkqsrddaalggm 240
 241 FMYELRGSLEPMOGLKADTLKERYOKIDTRKNTPIEALCENFPEMATYLRVYRRLDFE 300
 241 fmyelrgslepmoglkadtlkeryokidtrkntpiealcenfpeматыlrvyrrldffe 300
 301 KPDEYILRTLFITDLFEKKGITFDYAYRWGRRPTPYGSHVDSGASATIRESTHNDP 360
 301 kpdeyilrtlfitdlfekkgitfdyayrwgrrptpygshvdsagasatiressthndp 360
 361 SQOQPLRN-----QVSSSTNGELNVD 383
 361 sqoqplrn-----qvssstngelnvddp 420
 384 TGAHNAPIPTAHAEVEVEEAKCCCFEKKRRKRTAQRNK 422
 421 tgaahnapiptahaeveveeakcccfekrrkrtktaqgkh 459

RESULT 4
ID AAB97904 standard; Protein: 438 AA.
XX AAB97904;
AC AAB97904;
XX 10-AUG-2001 (first entry)
DT
XX
DE Human casein kinase 48 protein SEQ ID NO:2.
XX
XX
KW Human: casein kinase 48; cytosolic; immunomodulatory; antiinflammatory;
KW vitruicide; gene therapy; diagnosis; treatment; malignant tumour;
KW haemopathy; HIV infection; immunological disease; inflammation.
XX
OS Homo sapiens.
XX
PN WO200129228-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-CN00330.
XX
PR 18-OCT-1999; 99CN-0116987.
XX
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
XX
PI Mac Y, Xle Y;
XX
DR WPI: 2001-282163/29.
DR N-PSDB: AAH21501.
XX
XX
PT Human casein kinase 48 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation -
XX
XX
PS Claim 1; Page 23-24; 30pp; Chinese.
XX
XX
CC The present sequence represents human casein kinase 48 (CK48). CK48 has
CC cytosolic, immunomodulatory, antiinflammatory and vitruicide activity,
CC and can be used in gene therapy. The CK48 protein and polynucleotide
CC sequences can be used in the diagnosis and treatment of malignant
CC tumour, haemopathy, HIV infection, immunological diseases and various
CC inflammation.
XX
XX
SQ Sequence 438 AA;
Query Match 96.0%; Score 2157; DB 22; Length 438;
Best Local Similarity 99.0%; Pred. No. 3.2e-221;
Matches 407; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 MDHRSREKDERQRTTKPAORSAHCSRPSGSSSSGVLMVGNPFVGGKIGCGNGEIRL 60
Db 1 mdhpsrekdqrctkpnagrsancstpsgsssgvilmvgnptfrvgkklcgngelrl 60
OY 61 GKNLYTNEYVAIKLEPIKSRAPOLALEYRFYKOLGSAGEGLPOVYFFGPGCKYNNMAYEL 120
Db 61 gknlytneyvaiklepiksrappqlhleyrfykqigsageglpvyvffpgckkynamvel 120
OY 121 LGSFLEDFLDCDRFTITKTYLMTAQLLSRMEYVHSKNLIYRDYKPNFLIGROGNKE 180
Db 121 lgsfledfldcdrtfcltkvltmalaqllsrmeyvhsknliyrdivkpenfligrgnke 180
OY 181 HVHIDHGLAKKEYIDPETKHIPREKSLTGTARYKSIWTHLGKESRRDDLEALGHM 240
Db 181 hvhldhglakeyidpetkhipreksltgtarymsintthlgkesrrddlealghm 240
OY 241 FMYFLRGSIPWQGLKADTLKERYOKIGDTKRNTPLEALCENFPPEMATYLRVYRRLDFE 300
Db 241 fmyflrsgslpwqglkadtlkerykigdtkrntplealcenfpemategyrvrrldffe 300

OY 301 KPDYELRLTFLDLEFKKGYTFDYAYDWVGRPIPTPVGSVVDGASATRESHTHRDP 360
Db 301 kpdyeylrltfltdlefkkytfdyaydwvgrpdpvgsvvdgsasaltreshthdrp 360
OY 361 SGOOPLRNQVVSSTNGELNVDDPTGAHSNAPITAAEVEVEAKCCFFK 411
Db 361 sgqoplrnqvvsstngelnvddptgahsnapitaaevveeakcclmfk 411
RESULT 5
ID AAR56529 standard; Protein: 377 AA.
XX AAR56529;
AC AAR56529;
XX 17-MAR-1995 (first entry)
DT
XX
DE Protein kinase (CKigamma1hu).
XX
XX
KW Protein kinase; immunogen; antibody; protein-tyrosine kinase;
KW protein-serine/threonine kinase; recombination; repair; screening;
KW detection; casein kinase.
XX
OS Homo sapiens.
XX
PN WO9417189-A.
XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US00795.
XX
PR 21-JAN-1993; 93US-0008001.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Hoekstra MF;
XX
DR WPI: 1994-264102/32.
DR N-PSDB: AAO56529.
XX
XX
PT Wild-type and mutant protein kinase genes and encoded
PT polypeptide(s) - Useful in screening for compositions which may
PT effect DNA double strand break repair activity
XX
XX
PS Claim 11; Page 100-101; 121pp; English.
XX
XX
CC This sequence is a protein kinase similar to the HRR25 protein of
CC Saccharomyces cerevisiae which is described in AAR56519.
CC Host cells stably transformed with the protein kinase encoding DNA
CC may be used for the expression of the protein kinase such that the
CC expressed protein is "displayed" on the host cell surface. The
CC cells may then be used as immunogen for the production of antibodies.
CC The host cells may also be used for the large scale production of the
CC protein kinase, the expressed protein being either isolated from the
CC cell surface or from the culture medium. Recombinant HRR25 like
CC proteins display a number of properties which are unique among the
CC eukaryotic protein kinases e.g. the HRR25 protein possesses both
CC protein-tyrosine kinase and protein-serine/threonine kinase
CC activities. Also, HRR25 operates to promote repair of DNA strand
CC breaks at a specific nucleotide sequence and is the only protein
CC kinase known to have such recombination/repair promoting activity.
CC Recombinant HRR25-like proteins and host cells expressing them are
CC useful in screening methods designed to examine the effects of
CC various compositions on DNA break repair and protein kinase
CC activities of the protein. The HRR25-like proteins are casein
CC kinase class I protein kinases.
XX
XX
SQ Sequence 377 AA;
Query Match 74.3%; Score 1669.5; DB 15; Length 377;
Best Local Similarity 84.8%; Pred. No. 3e-169;
Matches 318; Conservative 21; Mismatches 27; Indels 9; Gaps 5;

Oy	21	NSAHSRSGSSSSSSGVLMAVGNPNRVGKKTIGCGNFGELRLGKKNLTNEYVAIKTEPIKSR	80
Dd	7	tsghntcgtc-sssgvltmwpnltvgkklgcnlfgelrrlgknlytneyvalklepmkr	65
Oy	81	APOLHLEEFKFKOLGSAGEGLPQVYVYVPGCGKNYANVLELGLPSLEDLPDLCDRTFFIKT	140
Dd	66	apqhlleyrf/kqjys-gdglpdyvylfpgpcgkyamwvlellgplledlfdlcdrtfslkt	124
Oy	141	VLMATLQLLSMWEVYHSAKNIILRYOVKEENFLIGQGNKKKEHYIHIDFGAKETIDPETK	200
Dd	125	vmlatqlqlstmevvhsknlllyirldvknpenflilgprgnktqgvhlildlfglaketyldepk	184
Oy	201	KHIFPERKSLTGTARYKSIINTHGLKQSRDDLEALGHMFVFLRSGSLPMOGHKADTLK	260
Dd	185	khlfperkshltgtarymslnthlgkqsrddlealghmfvlrslgslpmogkadtik	244
Oy	245	eryqglgtktratlrvlelcnfpeematyltrvyrldlffekpdyrlrkltfdlfdarky	304
Dd	305	mldyewdlvgqltcltpygaavqgdplals-nreaqhrlckmqgs---knqvssstngeln	360
Oy	381	DDPTG---AHSNAPI 392	
Dd	361	ddptadvgmhpsqpi 375	
RESULT	6		
AAAR76625	ID	AAAR76625 standard; Protein; 377 AA.	
XX	XX	AAAR76625;	
XX	DT	25-JAN-1996 (first entry)	
XX	XX	Human HRR25-like casein-kinase-I CK1-gamma-1Hu protein.	
XX	XX		
KW	KW	Casein-kinase-I, HRR25; protein-tyrosine-kinase; CK1-gamma-1Hu;	
KM	KM	Protein-serine/threonine-kinase; enzyme; DNA repair;	
XX	XX	DNA recombination.	
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	MO9519993-A1.	
XX	PD	27-JUL-1995.	
XX	PF	23-JAN-1995; 95MO-US00955.	
XX	PR	21-JAN-1994; 94US-0185359.	
XX	PA	(SALK) SALK INST BIOLOGICAL STUDIES.	
XX	PI	Hoekstra MF;	
DR	DR	WPI: 1995-269419/35.	
XX	XX	N-PSDB; AAQ92962.	
PT	PT	New monoclonal antibodies against human casein Kinase Class I	
PT	PT	enzymes - useful for purification, and determin. of these enzymes and to	
XX	XX	modulate their receptor -ligand binding, also new hybridomas	
XX	PS	Disclosure; Page 100; 125pp; English.	
XX	XX		
CC	CC	This human casein-kinase-I (CKI-gamma-1Hu) protein which is a homolog	
CC	CC	of a DNA recombination and repair protein HRR25 (HO and/or	
CC	CC	radiation repair) possesses both protein-tyrosine-kinase and protein	
CC	CC	serine/threonine-kinase activities. HRR25 operates to promote repair	
CC	CC	of DNA strand breaks at a specific nucleotide sequence and is the	
CC	CC	only protein-kinase known to have such recombination/repair	

CC	promoting activity.	
XX	Sequence	377 AA:
XX	Query Match	74.3%; Score 1669.5; DB 16; Length 377;
XX	Best Local Similarity	84.8%; Pred. No. 3e-169;
XX	Matches 318; Conservative	21; Mismatches 27; Indels 9; Gaps 5;
QY	21	RSAHCSRPSGSSSSGVLWGPENFRVGRKIGCGNFGLRLGNLYTNEYVAIKLEPIKSR 80
DB	7	rsghntcrlgtg-ssssgvlmwgpnfrfvgkkligcgnfgeirlrgknllytneyvalklepmksr 65
QY	81	APQLHLERFRFYKQLGSAGEGLPQVYYFFPGCGKYNMAYLELLGPSLEDLFDLCDFRTFLKT 140
DB	66	apqhlleyrfykqlgs-gdglpvyvyfgpgckynamvalellgpsledlfdlcdrtflsikt 124
QY	141	VLMIAIOLLSRREYVHSKNLYRDVKNPENFLIRGCGNKEHVIHIDFLAKEVITDPEPK 200
DB	125	vlmiaiaqlistmemyhsknlllyrdvknpenflirgpnktqyinhldfglakeyldpetk 184
QY	201	KHIEVREHKSITGTARAYMSINTHLGKEOSRRDLEFALGMEMYFLRGSIPMOGLKADTLK 260
DB	185	khieprehksitgtaraysinthlgkegsrrddlealghmfmlyflrsglpmgyladtlk 244
QY	261	ERYQKIGTCKRNTPIEALCENPREMATYLRVRRLDFFEKRDYELNTLFTDFEKKGY 320
DB	245	eryqkigtcktrntpiealcenprematylrvrrldffekrpylrlkklftdldftrkgy 304
QY	321	TEFDAVMDVNGRPIRPVGSVHVDSASAITRESHNHRDRPQOQPLRNOVVSSTNGELNV 380
DB	305	mfdeydwldvngqirpvpavagqdpals-areahqhrdkmgqs--knqvssstngelnt 360
QY	381	DDPTG---AHSNAPI 392
DB	361	ddptcdvqmhpsqpl 375
RESULT	7	
AA	AA56530	
ID	AA56530	standard; Protein: 347 AA.
XX	AA56530:	
XX	17-MAR-1995	(first entry)
XX	DE	Protein kinase (CKIgamma2Hu).
XX	KW	Protein kinase; immunogen; antibody; protein-tyrosine kinase;
XX	KM	protein-serine/threonine kinase; recombination; repair; screening;
XX	OS	detection; casein kinase.
XX	XX	Homo sapiens.
XX	XX	W09417189-A.
XX	XX	04-AUG-1994.
XX	XX	21-JAN-1994; 94MO-US00795.
XX	XX	21-JAN-1993; 93US-0008001.
XX	XX	(SALK) SALK INST BIOLOGICAL STUDIES.
XX	XX	Hoekstra MF;
XX	XX	PI
XX	XX	WPI, 1994-264102/32.
XX	XX	N-PSDB; AAO70828.
XX	XX	Wild-type and mutant protein kinase genes and encoded
XX	XX	PT polypeptide(s) - useful in screening for compositions which may
XX	XX	effect DNA double strand break repair activity

PS Claim 11; Page 103-104; 121pp; English.

XX This sequence is a protein kinase similar to the HRR25 protein of

CC *Saccharomyces cerevisiae* which is described in AAR56519.

CC Host cells stably transformed with the protein kinase encoding DNA

CC may be used for the expression of the protein kinase such that the

CC expressed protein is "displayed" on the host cell surface. The

CC cells may then be used as immunogen for the production of antibodies.

CC The host cells may also be used for the large scale production of the

CC protein kinase, the expressed protein being either isolated from the

CC cell surface or from the culture medium. Recombinant HRR25 like

CC proteins display a number of properties which are unique among the

CC eukaryotic protein kinases e.g. the HRR25 protein possesses both

CC protein-tyrosine kinase and protein-serine/threonine kinase

CC activities. Also, HRR25 operates to promote repair of DNA strand

CC breaks at a specific nucleotide sequence and is the only protein

CC kinase known to have such recombination/repair promoting activity.

CC Recombinant HRR25-like proteins and host cells expressing them are

CC useful in screening methods designed to examine the effects of

CC various compositions on DNA break repair and protein kinase

CC activities of the protein. The HRR25-like proteins are casein

CC kinase class I protein kinases.

XX

SO Sequence 347 AA;

Query Match 69.9%; Score 1571.5; DB 15; Length 347;

Best Local Similarity 84.9%; Pred. No. 7.7e-159;

Matches 298; Conservative 19; Mismatches 25; Indels 9; Gaps 5;

QY 45 RVGKKGCGNGELRLGNLTNEVAIKLEPIKSRAPQLHLEFYFQOLGSGGLPOV 104

DB 1 RVGKKGCGNGELRLGNLTNEVAIKLEPIKSRAPQLHLEFYFQOLGSGGLPOV 59

QY 105 YVFGPCGYKYMVLELPSLEDLEDCRFTFTKTVLMAIQLSRMEYVSKNLIYRD 164

DB 60 YVFGPCGYKYMVLELPSLEDLEDCRFTFTKTVLMAIQLSRMEYVSKNLIYRD 119

QY 165 VKPENFLIGROGKNEHVIHIDFGLAKEYIDPETKKHPIREKSLGTARVMSINTHL 224

DB 120 VKPENFLIGROGKNEHVIHIDFGLAKEYIDPETKKHPIREKSLGTARVMSINTHL 179

QY 225 GKESRRDDELALGHMFYFIRGSLPMOGLKADITKERYKIGDKRNTPIEALCENPPE 284

DB 180 GKESRRDDELALGHMFYFIRGSLPMOGLKADITKERYKIGDKRNTPIEALCENPPE 238

QY 285 EMATYLRVRLDPEFEKPDYELRLFTDLFEKKGYTFDVAYDVGRIPIPVGSHVDS 344

DB 239 EMATYLRVRLDPEFEKPDYELRLFTDLFEKKGYTFDVAYDVGRIPIPVGSHVDS 298

QY 345 GASAITRESHTHRDRPSQOQLRNQVYSTNGELNVDDPTG--AHSNAPI 392

DB 299 aals-nreahqhrdkmgs--knqvssstngelntddprtdvqmhpsqpl 345

RESULT 8

AAR76626 ID AAR76626 standard; Protein: 347 AA.

XX AAR76626;

AC AAR76626;

XX

DT 25-JAN-1996 (first entry)

XX

DE Human HRR25-like casein-kinase-I CK1-gamma-2Hu protein.

XX

KW Casein-kinase-I; HRR25; protein-tyrosine-kinase; CK1-gamma-2HU;

KM protein-serine/threonine-kinase; enzyme; DNA repair;

KW DNA recombination.

XX

XX Homo sapiens.

OS

XX

PN W09519993-A1.

XX

PD 27-JUL-1995.

XX

PF 23-JAN-1995; 95WO-US00955.

XX

PR 21-JAN-1994; 94US-0185359.

XX

PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX

PI Hoechst MF;

XX

DR WPI: 1995-269419/35.

DR N-PSDB: AAQ92963.

XX

PT New monoclonal antibodies against human casein kinase class I

PT enzymes - useful for purification, and determin. of these enzymes and to

PT modulate their receptor -ligand binding; also new hydridomas

XX

PS Disclosure; Page 104; 125pp; English.

XX

CC This human casein-kinase-I (CK1-gamma-2Hu) protein which is a homolog

CC of a DNA recombination and repair protein HRR25 (HO and/or

CC radiation repair) possesses both protein-tyrosine-kinase and protein

CC serine/tyrosine-kinase activities. HRR25 operates to promote repair

CC of DNA strand breaks at a specific nucleotide sequence and is the

CC only protein-kinase known to have such recombination/repair

CC promoting activity.

CC

XX

SO Sequence 347 AA;

Query Match 69.9%; Score 1571.5; DB 16; Length 347;

Best Local Similarity 84.9%; Pred. No. 7.7e-159;

Matches 298; Conservative 19; Mismatches 25; Indels 9; Gaps 5;

QY 45 RVGKKGCGNGELRLGNLTNEVAIKLEPIKSRAPQLHLEFYFQOLGSGGLPOV 104

DB 1 RVGKKGCGNGELRLGNLTNEVAIKLEPIKSRAPQLHLEFYFQOLGSGGLPOV 59

QY 105 YVFGPCGYKYMVLELPSLEDLEDCRFTFTKTVLMAIQLSRMEYVSKNLIYRD 164

DB 60 YVFGPCGYKYMVLELPSLEDLEDCRFTFTKTVLMAIQLSRMEYVSKNLIYRD 119

QY 165 VKPENFLIGROGKNEHVIHIDFGLAKEYIDPETKKHPIREKSLGTARVMSINTHL 224

DB 120 VKPENFLIGROGKNEHVIHIDFGLAKEYIDPETKKHPIREKSLGTARVMSINTHL 179

QY 225 GKESRRDDELALGHMFYFIRGSLPMOGLKADITKERYKIGDKRNTPIEALCENPPE 284

DB 180 GKESRRDDELALGHMFYFIRGSLPMOGLKADITKERYKIGDKRNTPIEALCENPPE 238

QY 285 EMATYLRVRLDPEFEKPDYELRLFTDLFEKKGYTFDVAYDVGRIPIPVGSHVDS 344

DB 239 EMATYLRVRLDPEFEKPDYELRLFTDLFEKKGYTFDVAYDVGRIPIPVGSHVDS 298

QY 345 GASAITRESHTHRDRPSQOQLRNQVYSTNGELNVDDPTG--AHSNAPI 392

DB 299 aals-nreahqhrdkmgs--knqvssstngelntddprtdvqmhpsqpl 345

RESULT 9

ABB66550 ID ABB66550 standard; Protein: 422 AA.

XX ABB66550;

AC ABB66550;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 26442.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

KM pharmaceutical.

XX

OS Drosophila melanogaster.

XX WO200171042-A2.
PN 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PMD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL10653.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 26442; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 422 AA:
SO
Query Match 69.1%; Score 1553; DB 22; Length 422;
Best Local Similarity 70.8%; Pred. No. 9,8e-157;
Matches 294; Conservative 41; Mismatches 52; Indels 28; Gaps 4;
OY 32 SSSSGVLMVGNPNRVGKKGNGELRLGKNLYTNEYVAIKLEPIKSRAPOLHLEVRFY 91
DB 9 sttgytlmvgpnfrivgkkgngelrlgknlytneyvaiklepiksrappolhletryfy 68
OY 92 KOLGSAEGELPOVYFEGPCGKYNAMVELLGPSELEDFDLCDRTFTLTKVTMLAIOQLSR 151
DB 69 kllyghnaegvpevyfyfpgckynalvmellgpledfdlcgrtrfltksvlllaigllhr 128
OY 152 MEVYHSKNLIYRDVKNPBNFLIGROGKKEHVHITDFGLAKKEYIDPETKHHIPYREHKS 211
DB 129 leyvhsrhllyrtdvknpenfligrtstkreklhldfglakeyldldtnhlyprehksl 188
OY 212 TGTARVMSINTHGHKEGSRDDEALGHPMFYLRGSLPMOGKADPLKRRYOKIGPTR 271
DB 189 tgarvmsintthghkegsrddlealghpmfmylrgslpmsgkadtllkeryqkldqctr 248
OY 272 NPTIEALCENFPEEMATYLYRVRLDFFEKPDYEYLTLETDLEFKKGYFDAYDWVGR 331
DB 249 atplevldcghpneefatyllyrvrldffetpdydflrrlqgdlfdtrkygdegefdwtgk 308
OY 332 PIRTPVGSVHVDGASAI---TRESH-----THRRPSGOQPLRN----- 368
DB 309 tmsrtpvgs--lqtshevlispnkdrlhntaktakgsvaaapdvpxpगतलiltpadrlh 366
OY 369 ---OVASTNGELNVDDPGTGAHSNAPITAAEYVEAEKCCCFKKRKKRKTQR 420
DB 367 gsvavvstngelnvddpgtgaahsnaptitaaeyveaeakcccfkkkkkstrq 421
RESULT 10
ABBS71525

ID ABB71525 standard; Protein: 422 AA.
XX ABB71525;
AC 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 41367.
DT
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 41367.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PMD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL15628.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 41367; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 422 AA:
SO
Query Match 69.1%; Score 1553; DB 22; Length 422;
Best Local Similarity 70.8%; Pred. No. 9,8e-157;
Matches 294; Conservative 41; Mismatches 52; Indels 28; Gaps 4;
OY 32 SSSSGVLMVGNPNRVGKKGNGELRLGKNLYTNEYVAIKLEPIKSRAPOLHLEVRFY 91
DB 9 sttgytlmvgpnfrivgkkgngelrlgknlytneyvaiklepiksrappolhletryfy 68
OY 92 KOLGSAEGELPOVYFEGPCGKYNAMVELLGPSELEDFDLCDRTFTLTKVTMLAIOQLSR 151
DB 69 kllyghnaegvpevyfyfpgckynalvmellgpledfdlcgrtrfltksvlllaigllhr 128
OY 152 MEVYHSKNLIYRDVKNPBNFLIGROGKKEHVHITDFGLAKKEYIDPETKHHIPYREHKS 211
DB 129 leyvhsrhllyrtdvknpenfligrtstkreklhldfglakeyldldtnhlyprehksl 188
OY 212 TGTARVMSINTHGHKEGSRDDEALGHPMFYLRGSLPMOGKADPLKRRYOKIGPTR 271
DB 189 tgarvmsintthghkegsrddlealghpmfmylrgslpmsgkadtllkeryqkldqctr 248
OY 272 NPTIEALCENFPEEMATYLYRVRLDFFEKPDYEYLTLETDLEFKKGYFDAYDWVGR 331
DB 249 atplevldcghpneefatyllyrvrldffetpdydflrrlqgdlfdtrkygdegefdwtgk 308

[illegible]

```

PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155485.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

Query Match 41.7%; Score 938; DB 21; Length 476;
 Best Local Similarity 54.2%; Pred. No. 5.8e-91;
 Matches 180; Conservative 60; Mismatches 84; Indels 8; Gaps 5;

```

QY 38 LMGVNFVGGKKGCGNGELRLGNLYTNEVAIKLEPIKSRAPQDLHLEFRFYQLGSA 97
DB 3 lviqgkfkigkigsgsfgylylgvavgtgeevavklevkthqplhyesklyml-qg 61
QY 98 GEGLPQVYVFGPCGKYNNMVELLGPSEDLFDLDRFTTKTYMIAIQLSRMEYVHS 157
DB 62 gsglpnlkwiqvgdyvawidllpsiedlfnycnrkltkltvmladqllnvefmht 121
QY 158 KNLIVRDVKNPENFLIGROGNKKEHYIHIDFLAKKEYIDPEPKKHIPYREKSLTGARY 217
DB 122 rglfhrdtkpndflmg1--gktangvylidfglgkkyrdlqthkhlpyrenknlgtary 179
QY 218 MSINTHLCKEQRDDLEALGHMFWYFLRGLSPWOGKADLTKEKRYOKIGTKRNTPIEA 277
DB 180 asvthlqvegsirdldslslyvlnmyflkgsipwglkagtkkgydrisekkvstplev 239
QY 278 LCENPEEMATYLYRVRLDPEFEKPDYELRTLEFDLEFEKKGYPDYVDMWGRIPRPV 337
DB 240 lcknqpselvfynycslrfdckpdylylkrllfdlfliregylqyfdwcvlkyrp-q1 298
QY 338 GSVHVDGASATRESHTHRDRPSGOQPLRNO 369
DB 299 gs---ssgsssrth-hltakpgfnadplerg 326

```

RESULT 13
 AAR56531
 ID AAR56531 standard; Protein; 415 AA.
 XX
 AC AAR56531;

```

XX 17-MAR-1995 (first entry)
DT
XX Protein kinase (CKIdeltaHu).
DE
XX Protein kinase; immunogen; antibody; protein-tyrosine kinase;
KW protein-serine/threonine kinase; recombination; repair; screening;
KW detection; casein kinase.
OS
XX Homo sapiens.
XX WO9417189-A.
XX 04-AUG-1994.
PD
XX 21-JAN-1994; 94MO-US00795.
PF
XX 21-JAN-1993; 93US-0008001.
PR
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX Hoekstra ME;
XX WPL 1994-264102/32.
XX N-PSDB; AA070829.
DR
XX Wild-type and mutant protein kinase genes and encoded
PT polypeptide(s) - useful in screening for compositions which may
PT effect DNA double strand break repair activity
PS
XX Claim 11; Page 107-108; 121pp; English.
XX
XX This sequence is a protein kinase similar to the HRR25 protein of
CC Saccharomyces cerevisiae which is described in AAR56519.
CC Host cells stably transformed with the protein kinase encoding DNA
CC may be used for the expression of the protein kinase such that the
CC expressed protein is "displayed" on the host cell surface. The
CC cells may then be used as immunogen for the production of antibodies.
CC The host cells may also be used for the large scale production of the
CC protein kinase, the expressed protein being either isolated from the
CC cell surface or from the culture medium. Recombinant HRR25 like
CC proteins display a number of properties which are unique among the
CC eukaryotic protein kinases e.g. the HRR25 protein possesses both
CC protein-tyrosine kinase and protein-serine/threonine kinase
CC activities. Also, HRR25 operates to promote repair of DNA strand
CC breaks at a specific nucleotide sequence and is the only protein
CC kinase known to have such recombination/repair promoting activity.
CC Recombinant HRR25-like proteins and host cells expressing them are
CC useful in screening methods designed to examine the effects of
CC various compositions on DNA break repair and protein kinase
CC activities of the protein. The HRR25-like proteins are casein
CC kinase_class I protein kinases.
XX
XX Sequence 415 AA;
SO

```

Query Match 41.6%; Score 936; DB 15; Length 415;
 Best Local Similarity 47.2%; Pred. No. 7.7e-91;
 Matches 186; Conservative 75; Mismatches 97; Indels 38; Gaps 6;

```

QY 38 LMGVNFVGGKKGCGNGELRLGNLYTNEVAIKLEPIKSRAPQDLHLEFRFYQLGSA 97
DB 3 lviqgkfkigkigsgsfgylylgdlaageavklcecvtkhqp1hiesklykmm-qg 61
QY 98 GEGLPQVYVFGPCGKYNNMVELLGPSEDLFDLDRFTTKTYMIAIQLSRMEYVHS 157
DB 62 gvglpnlrwcgaegdynmwemllpsiedlfnfcsrfskltvllladqmslreyhs 121
QY 158 KNLIVRDVKNPENFLIGROGNKKEHYIHIDFLAKKEYIDPEPKKHIPYREKSLTGARY 217
DB 122 knfhrdvkpnflmg1--gktgnlyvylidfglakkydarthqhlpyrenknlgtary 179
QY 218 MSINTHLCKEQRDDLEALGHMFWYFLRGLSPWOGKADLTKEKRYOKIGTKRNTPIEA 277

```

```

Db 180 aslnhlgtesrirdleslyvumyfnlsglpgkaatkqkyerisekkmsuplev 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 278 LCNENPEEMAAVLRVVRRLDPEFEKQDEYVETLTETDLEKKGYTFDYAVYMGSRPIPTPV 337
      ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 240 lckypsefaelylfcslrlfddkpdpsylqlrlmfnhpgfsydyfaw----- 280
      ||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Oy 338 GSVHNDOSASATRESHTRHRRPESQOQPLRNQVYSSTNG-----ELNVDPT 384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 291 -nmkfkfjasaadaa-eteridreelrlnsmptarlglpstasgrlrgtqevapptrl 346
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 385 GAHSNAPITTAHEVEVEEAKCCCFPRKRKKTKAQRK 422
      ||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 347 tptshantstprpvsyme-----tekvsmrlnhr 375
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

[illegible]

PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: August 17, 2002, 19:23:15 ; Search time 24.87 seconds
(without alignments)
414.459 Million cell updates/sec

Title: US-09-765-068-2

Perfect score: 2248
Sequence: 1 MDHPSREKREKRTTKPMQA.....EAKCCCFKRRKKTQRHK 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1669.5	74.3	377	1	US-08-454-097-31 Sequence 31, Appl
2	1669.5	74.3	377	3	US-08-185-359-31 Sequence 31, Appl
3	1571.5	69.9	347	1	US-08-454-097-33 Sequence 33, Appl
4	1571.5	69.9	347	3	US-08-185-359-33 Sequence 33, Appl
5	946.5	42.1	416	3	US-09-100-664A-9 Sequence 9, Appl
6	936	41.6	415	1	US-08-454-097-35 Sequence 35, Appl
7	936	41.6	415	3	US-08-185-359-35 Sequence 35, Appl
8	924	41.1	365	1	US-08-447-500-4 Sequence 4, Appl
9	924	41.1	365	3	US-08-454-097-4 Sequence 4, Appl
10	924	41.1	365	1	US-08-453-866-4 Sequence 4, Appl
11	924	41.1	365	3	US-09-100-664A-13 Sequence 13, Appl
12	924	41.1	365	3	US-08-185-359-4 Sequence 4, Appl
13	923.5	41.1	319	3	US-09-100-664A-10 Sequence 10, Appl
14	907.5	40.4	400	1	US-08-447-500-6 Sequence 6, Appl
15	907.5	40.4	400	1	US-08-454-097-6 Sequence 6, Appl
16	907.5	40.4	400	1	US-08-453-866-6 Sequence 6, Appl
17	907.5	40.4	400	1	US-08-185-359-6 Sequence 6, Appl
18	884	39.3	440	3	US-09-100-664A-2 Sequence 2, Appl
19	880	39.1	440	3	US-09-100-664A-4 Sequence 4, Appl
20	876	39.0	440	3	US-09-100-664A-3 Sequence 3, Appl
21	862.5	38.4	325	1	US-08-447-500-8 Sequence 8, Appl
22	862.5	38.4	325	1	US-08-454-097-8 Sequence 8, Appl
23	862.5	38.4	325	1	US-08-453-866-8 Sequence 8, Appl
24	862.5	38.4	325	3	US-08-185-359-8 Sequence 8, Appl
25	862.5	38.4	337	1	US-08-447-500-10 Sequence 10, Appl
26	862.5	38.4	337	1	US-08-454-097-12 Sequence 12, Appl
27	862.5	38.4	337	1	US-08-453-866-10 Sequence 10, Appl

28	862.5	38.4	337	3	US-09-100-664A-11 Sequence 11, Appl
29	862.5	38.4	337	3	US-09-100-664A-12 Sequence 12, Appl
30	862.5	38.4	337	3	US-08-185-359-12 Sequence 12, Appl
31	860.5	38.3	494	1	US-08-447-500-2 Sequence 2, Appl
32	860.5	38.3	494	1	US-08-454-097-2 Sequence 2, Appl
33	860.5	38.3	494	1	US-08-447-408-2 Sequence 2, Appl
34	860.5	38.3	494	1	US-08-453-866-2 Sequence 2, Appl
35	860.5	38.3	494	3	US-08-185-359-2 Sequence 2, Appl
36	847.5	37.7	364	1	US-08-447-500-12 Sequence 12, Appl
37	847.5	37.7	364	1	US-08-454-097-10 Sequence 10, Appl
38	847.5	37.7	364	1	US-08-453-866-12 Sequence 12, Appl
39	847.5	37.7	364	3	US-08-185-359-10 Sequence 10, Appl
40	800	35.6	524	1	US-08-447-500-24 Sequence 24, Appl
41	800	35.6	524	1	US-08-454-097-24 Sequence 24, Appl
42	800	35.6	524	1	US-08-453-866-24 Sequence 24, Appl
43	800	35.6	524	3	US-08-185-359-24 Sequence 24, Appl
44	326.5	14.5	396	2	US-08-878-989-16 Sequence 16, Appl
45	326.5	14.5	396	4	US-09-272-796-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-454-097-31
Sequence 31, Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-097-31
Query Match 74.3%; Score 1669.5; DB 1; Length 377;

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-097-33

Query Match 69.9%; Score 1571.5; DB 1; Length 347;
Best Local Similarity 84.9%; Pred. No. 2,2e-151;
Matches 298; Conservative 19; Mismatches 25; Indels 9; Gaps 5;

OY 45 RVGKIGCGNGELRLGKNTYNEVAIKLEPIKSRAPQLHLEFRFYQLSGAGELPOV 104
DB 1 RVGKIGCGNGELRLGKNTYNEVAIKLEPIKSRAPQLHLEFRFYQLSGAGELPOV 59
OY 105 YFGPGCKYNAVLELLGPSLEDFLDCDRTFTLKTVMIAIQLSRMEYHSHKLLIYRD 164
DB 60 YFGPGCKYNAVLELLGPSLEDFLDCDRTFTLKTVMIAIQLSRMEYHSHKLLIYRD 119
OY 165 VKPENFLIGROGKKEHYIHIDFLGKEYIDPETKKHIPPYREHKSLSGTARYSINTHL 224
DB 120 VKPENFLIGROGKKEHYIHIDFLGKEYIDPETKKHIPPYREHKSLSGTARYSINTHL 179
OY 225 GKEOSRRDLDALGHMEYFLRGSIPMOGLKADTLKERYOKIGDKRNTPIEALCENPE 284
DB 180 GKEOSRRDLDALGHMEYFLRGSIPMOGLKADTLKERYOKIGDKRNTPIEALCENPE 238
OY 285 EMATYLRVRLDFFEKEDYEYLTFTLDFEKKGYTFDYAYDWGRIPTPVGSVHDS 344
DB 239 EMATYLRVRLDFFEKEDYEYLTFTLDFEKKGYTFDYAYDWGRIPTPVGSVHDS 298
OY 345 GASAITRESHTHRRSPSOQPLRNQVSSSTNGELNVDDPTG---AHSNAPI 392
DB 239 ALSS-NREAHQRDKMOOS---KNQVSSSTNGELNVDDPTADYQMHPSQPL 345

RESULT 4
US-08-185-359-33
Sequence 33, Application US/08185359
Patent No. 6060296
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783

FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-185-359-33

Query Match 69.9%; Score 1571.5; DB 3; Length 347;
Best Local Similarity 84.9%; Pred. No. 2,2e-151;
Matches 298; Conservative 19; Mismatches 25; Indels 9; Gaps 5;

OY 45 RVGKIGCGNGELRLGKNTYNEVAIKLEPIKSRAPQLHLEFRFYQLSGAGELPOV 104
DB 1 RVGKIGCGNGELRLGKNTYNEVAIKLEPIKSRAPQLHLEFRFYQLSGAGELPOV 59
OY 105 YFGPGCKYNAVLELLGPSLEDFLDCDRTFTLKTVMIAIQLSRMEYHSHKLLIYRD 164
DB 60 YFGPGCKYNAVLELLGPSLEDFLDCDRTFTLKTVMIAIQLSRMEYHSHKLLIYRD 119
OY 165 VKPENFLIGROGKKEHYIHIDFLGKEYIDPETKKHIPPYREHKSLSGTARYSINTHL 224
DB 120 VKPENFLIGROGKKEHYIHIDFLGKEYIDPETKKHIPPYREHKSLSGTARYSINTHL 179
OY 225 GKEOSRRDLDALGHMEYFLRGSIPMOGLKADTLKERYOKIGDKRNTPIEALCENPE 284
DB 180 GKEOSRRDLDALGHMEYFLRGSIPMOGLKADTLKERYOKIGDKRNTPIEALCENPE 238
OY 285 EMATYLRVRLDFFEKEDYEYLTFTLDFEKKGYTFDYAYDWGRIPTPVGSVHDS 344
DB 239 EMATYLRVRLDFFEKEDYEYLTFTLDFEKKGYTFDYAYDWGRIPTPVGSVHDS 298
OY 345 GASAITRESHTHRRSPSOQPLRNQVSSSTNGELNVDDPTG---AHSNAPI 392
DB 239 ALSS-NREAHQRDKMOOS---KNQVSSSTNGELNVDDPTADYQMHPSQPL 345

RESULT 5
US-09-100-664A-9
Sequence 9, Application US/09100664A
Patent No. 6057129
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A


```

GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 568412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TEXT: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-097-4

Query Match 41.1%, Score 924; DB 1; Length 365;
Best Local Similarity 49.2%, Pred. No. 1.4e-85;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

```

```

Query Match 41.1%, Score 924; DB 1; Length 365;
Best Local Similarity 49.2%, Pred. No. 1.4e-85;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

374 TNGELN-----VDDP--TGA-HSNAP 391
Db 339 KCGDINTVPIYNDPSATGAQYINRP 364

RESULT 10
US-08-453-866-4
Sequence 4, Application US/08453866
Patent No. 5756289
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,866
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 20-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-866-4

Query Match 41.1%, Score 924; DB 1; Length 365;
Best Local Similarity 49.2%, Pred. No. 1.4e-85;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

```

Oy 158 KNLIRYRVPKPNFLIGQGNKKEHVHIIIDPLAKEIYDEPTKHIYREKSLTGARY 217
 Db 122 KNFTHRDVKNDFNLMGL--GKKGMLVYIIDFGLAKKRDARTHOIPIYREKKNLTGTARY 179
 Oy 218 MSINTHGLKESRRDDLEALGHPMFYLRGSLPWOGLKADTLKERYOKIGDTKKNPTIEA 277
 Db 180 ASINTHGLIGESRRDDLESGLVLMYFNLSLSPWOGLKATKROKRYISEKKKSTIEV 239
 Oy 278 LCNENPEEMATYLYRVRRLDFEFKPDYELRTLTFTDLFEKKGYTFDVAYDVGPIPTPV 337
 Db 240 LCKGYPEFATYLNFCRSLNFDDKPDYSYLRQLFRNLFFHQGFSDYVDFM----- 290
 Oy 338 GSVHVDGASATIRESTHHDPSQOOLPNQVYSTNG-----ELAVDDPT 384
 Db 291 --NMLKFGASRAADDA--EERERDRERLRHSRNPATGRLPSTASGRLRGTGVAPPTPL 346
 Oy 385 GASHNAPITAAEYVEVEAKCCCFKRRKRTAORHK 422
 Db 347 TPTSHNTANTSPRVSGME-----REKRVSHLRH 375

RESULT 8
 B86170
 ADK1 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: B86170
 R:Teoelogs, A.; Ecker, J. R.; Palm, C. J.; Federspiel, N. A.; Kaul, S.; White, O.; Alonso,
 Chin, C. W.; Chung, M. K.; Coml, L.; Conway, A. B.; Conway, A. R.; Creasy, T. H.; Dewar, K.;
 ansen, N. F.; Hughes, B.; Hutzler, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J. L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C. A.; Li, J. H.; Li, Y.; Lin, X.; Liu, S. X.; Liu, Z. A.; Luros, J. S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S. L.; Schwartz, J. R.; Shinn, P.; Southwick, A. M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C. M.; Venter, J. C.; Davis, R. W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; M0ID:21016719
 A:Accession: B86170
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-471 <STO>
 A:Cross-references: GB:AE005172; MID:g4204297; PIDN:GAD10678.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 41.2%; Score 927; DB 2; Length 471;
 Best Local Similarity 55.3%; Pred. No. 2.2e-48;
 Matches 176; Conservative 62; Mismatches 72; Indels 8; Gaps 5;
 Oy 38 LAMGNPFRVCKKICGCGFGLRGLKNTLYNEVAIKLEPIKSRAPOLHLEYRFGKQSGA 97
 Db 3 LVIGGKRLKRIKIGSGFGLYGLVGTNVAISEVAIKLESTRAPHOLEYRVRIL-SG 61
 Oy 98 GEGLPQYVYRPGCKYAMVLELGLPSLEDFDLCDRTFTLYKTVLMAIOLLSMEYVHS 157
 Db 62 GTGVNPKMGVGEDYANVMIIDGLPSLEDFLFCNKRKLKLYKTLMLADLINVVEPMHT 121
 Oy 158 KNLIRYRVPKPNFLIGQGNKKEHVHIIIDPLAKEIYDEPTKHIYREKSLTGARY 217
 Db 122 KNFTHRDVKNDFNLMGL--GKKGMLVYIIDFGLAKKRDARTHOIPIYREKKNLTGTARY 179
 Oy 218 MSINTHGLKESRRDDLEALGHPMFYLRGSLPWOGLKADTLKERYOKIGDTKKNPTIEA 277
 Db 180 ASINTHGLIGESRRDDLESGLVLMYFNLSLSPWOGLKATKROKRYISEKKKSTIEV 239
 Oy 278 LCNENPEEMATYLYRVRRLDFEFKPDYELRTLTFTDLFEKKGYTFDVAYDVGPIPTPV 337
 Db 240 LCKGYPEFATYLNFCRSLNFDDKPDYSYLRQLFRNLFFHQGFSDYVDFM----- 290
 Oy 338 GSVHVDGASATIRESTHHDPSQOOLPNQVYSTNG-----ELAVDDPT 384
 Db 291 --NMLKFGASRAADDA--EERERDRERLRHSRNPATGRLPSTASGRLRGTGVAPPTPL 346
 Oy 385 GASHNAPITAAEYVEVEAKCCCFKRRKRTAORHK 422
 Db 347 TPTSHNTANTSPRVSGME-----REKRVSHLRH 375

Db 299 GS---SSGSSRRR-NHT 312

RESULT 9

casein kinase-1 homolog hbp1 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 31-Jan-2000
 C:Accession: S46357; J02547; T04000; S44196
 R:Dillon, N.; Hoekstra, M. F.
 EMBO J. 13, 2777-2788, 1994
 A:Title: Characterization of two protein kinases from Schizosaccharomyces pombe Inv
 A:Reference number: S46357; M0ID:94298768
 A:Accession: S46357
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-365 <H1>
 A:Cross-references: EMBL:X78871; MID:g565629; PIDN:CAA55473.1; PID:g474400
 R:Keatney, P. H.; Edert, M.; Kurec, J.
 Blochem. Biophys. Res. Commun. 203, 231-236, 1994
 A:Title: Molecular cloning and sequence analysis of two novel fission yeast casein }
 A:Reference number: J02547; M0ID:94354807
 A:Accession: J02547
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-365 <KEA>
 A:Cross-references: EMBL:U01063; MID:g529901; PIDN:AAA21544.1; PID:g529902
 R:Lyne, M.; Rajadream, M. A.; Barrell, B. G.; Jimenez Martinez, J.
 Submitted to the EMBL Data Library, August 1998
 A:Reference number: 221926
 A:Accession: T04000
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-365 <LYN>
 A:Cross-references: EMBL:AL031261; PIDN:CAA20311.1; GSPDB:GN00067; SPDB:SPBC3H7.15
 A:Experimental source: strain 972h; cosmid c3H7
 C:Genetics:
 A:Gene: SPBC3H7.15
 A:Map position: 2
 A:Introns: 297/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 F;9-281/Domain: protein kinase homology <KIN>

Query Match 41.1%; Score 924; DB 2; Length 365;
 Best Local Similarity 49.2%; Pred. No. 2.4e-48;
 Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;
 Oy 38 LAMGNPFRVCKKICGCGFGLRGLKNTLYNEVAIKLEPIKSRAPOLHLEYRFGKQSGA 97
 Db 5 LRIGNKYRIGRKIGSGFGLYGLVGTNVAISEVAIKLESTRAPHOLEYRVRIL-SG 63
 Oy 98 GEGLPQYVYRPGCKYAMVLELGLPSLEDFDLCDRTFTLYKTVLMAIOLLSMEYVHS 157
 Db 64 GVGIPFRMGVGEDYANVMIIDGLPSLEDFLFCNKRKLKLYKTLMLADLINVVEPMHT 123
 Oy 158 KNLIRYRVPKPNFL--IGQGNKKEHVHIIIDPLAKEIYDEPTKHIYREKSLTGATA 215
 Db 124 KSFTHRDVKNDFNLMGLKRGNO---VNIIDGLAKKYDHTTHIPIYREKKNLTGTA 179
 Oy 216 RYMSINTHGLKESRRDDLEALGHPMFYLRGSLPWOGLKADTLKERYOKIGDTKKNPTI 275
 Db 180 RYASINTHGLIGESRRDDLESGLVLMYFNLSLSPWOGLKATKROKRYISEKKKSTIEV 239
 Oy 276 EALCENPEEMATYLYRVRRLDFEFKPDYELRTLTFTDLFEKKGYTFDVAYDVGPIPTPV 335
 Db 240 EVLCRGPQFSTYLNTRSLRFDKPDYALYKLFRLDFLCRSYSYEDVDFM----- 292
 Oy 336 PVGSHVDGASATIRESTHHDPSQOOLPNQVYSTNG-----ELAVDDPT 384
 Db 293 -----TLKRRKTOODOOHOOLOOOLASATPQAINPPERSFRNKOONFDE 338
 Oy 374 TNGELN-----VDDP--TGA-HSNAP 391

Db 339 KGGDINTVPVINDPSATGAQYINRP 364

RESULT 10

T43314

C:Species: Schizosaccharomyces pombe

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C/Accession: T43314; T37890

R:Kitamura, K.; Yamashita, I.

Gene 214, 131-137, 1998

A>Title: Identification of a novel casein kinase-1 homolog in fission yeast Schizosaccha

A/Reference number: Z22417; MID:98322261

A/Accession: T43314

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-439 <RT>

R:Rieger, M.; McDonough, R.C.; Rajandream, M.A.; Barrell, B.G.

Submitted to the EMBL Data Library, September 1999

A/Reference number: Z21752

A/Accession: T37890

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-439 <RT>

A/Cross-references: EMBL:AL117390; PIDN:CA55846.1; GSPDB:GND0066; SPDB:SPAC1805.05

A/Experimental source: strain 972h; cosmid c1805

C/Genetics:

A/Gene: ctk3; SPAC1805.05

A/Map position: 1

A/Intons: 45/3; 69/1; 118/3

Query Match

Best Local Similarity 41.1%; Score 924; DB 2; Length 439;

Matches 196; Conservative 63; Mismatches 126; Indels 40; Gaps 6;

QY 31 SSSSSGVLAMPNFRVCKKIGCGFGLRLGKNTYNEYVAIKLEPKSRAPDLHLYRF 90

Db 2 STSSHNVGVVHYRVKKGIGESFGMLFGVNLINQPIALKEKSRSEVPOLRDEYLT 61

QY 91 YKOGSAGEGLPOVYFPGCKKYANAVLELGPSELEDFDLCDRTFTKTYLMTAIOLLS 150

Db 62 YKLIMGL-PTGIPSYTYGEGSMYLVMDLIGSELEDFDYCGRRSPKTYAMIAKQMIT 120

QY 151 RMEYVHAKNLIYRDVKEPFLIGRGNKKKEVHIIDFGLAKEYIDETKKHPIREHKS 210

Db 121 RIQGVHHRHFIYRDKPNDFLIGPSPKTEVYAVDFGAKQYRDKTHVHRYPNEHKS 180

QY 211 LTGTARMSINTHLGKQSRDDEALGHNMFYFLKGSLEPMOGLKADTLKERYOKIDTK 270

Db 181 LSGTARMSINTHLGKQSRDDEALGHNMFYFLKGSLEPMOGLKADTLKERYOKIEKK 240

QY 271 RNPFEALCENPEEMATYLRVYRDLFEKPDVEYRTFTDFFKKGTFTDVAAYMV- 329

Db 241 QVTPLEKCEGYPKEETQYMIYARNLGYEAPDYDLSLFDLSLLRINETDQSKYDML 300

QY 330 ---GRPIPTFGSVHV-----DSGASAITRESHTRD--RPSQOQPLRNQVSS 373

Db 301 LNNKGWQYSAKQHVQRRHGTGNNRQSTIPYARTQNNLSSPSTPANNVVDAS 360

QY 374 T-----NGLNVDPTGHSNAPITAH-AEYEVYVEAKCCCFEK 411

Db 361 VATQKDIPIGRKASPQVQOQOQSSAQOQOPORVEOPAPOTPTOPTOQVTOAAAPAPSK 420

QY 412 KRRKK 416

Db 421 KSRKK 425

RESULT 11

A55661

protein kinase ADK1 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 10-Dec-1999

C/Accession: A55661

R:Ali, N.; Halfter, U.; Chua, N.H.

J. Biol. Chem. 269, 31626-31629, 1994

A>Title: Cloning and biochemical characterization of a plant protein kinase that phos

A/Reference number: A55661; MID:95081107

A/Accession: A55661

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A/Molecule type: mRNA

A/Residues: 1-319 <ALI>

A/Cross-references: GB:U48779; MID:q1216483; PIDN:AA847968.1; PID:q1216484

C/Superfamily: kinase-related transforming protein; protein kinase homology

F:7-279/Domains: protein kinase homology <KIN>

Query Match

Best Local Similarity 41.1%; Score 923.5; DB 2; Length 319;

Matches 174; Conservative 61; Mismatches 72; Indels 7; Gaps 4;

QY 38 LMGPNFRVCKKIGCGFGLRLGKNTYNEYVAIKLEPKSRAPDLHLYRFYKOGSA 97

Db 3 LVIGKFKLKRKIGSGFGLYLGINVOTGEVAVKLESVYTKRHPDLHYESKLYML-OG 61

QY 98 GEGLPVYFPGCKKYANAVLELGPSELEDFDLCDRTFTKTYLMTAIOLLSMEYVHS 157

Db 62 GTGPNKRWYGEVDVYVMDLIGPSELEDFENCKRSLKTYLMDQILNVEFMHT 121

QY 158 KNLIRDPVKEPFLIGRGNKKKEVHIIDFGLAKEYIDETKKHPIREHKS LGTARY 217

Db 122 RGLFHRDIPKPNFLMGL-GRKANQYIIDFGLEKKTARDQTHNHIYREKKNLTGTARY 179

QY 218 MSINTHLGKQSRDDEALGHNMFYFLKGSLEPMOGLKADTLKERYOKIGTKNTPEA 277

Db 180 ASVTHLGVGQSRDDEALGNYLMLKGSLEPMOGLKAGTKKOKYRISSEKVAIPLEV 239

QY 278 LCNFPEEMATYLRVYRDLFEKPDVEYRTFTDFFKKGTFTDVAAYDVGRPIRPV 337

Db 240 LCKNQSEYVYTRCNSLRFDDKPYDYLKRLRDLFIRGTFDYFDMVTLKYP-QI 298

QY 338 GSVHVDGASAITR 351

Db 299 GS---SSGSSSRTR 309

RESULT 12

T04626

probable protein kinase (EC 2.7.1.-) F2009.240 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 10-Dec-1999

C/Accession: T04626

R:Bevan, M.; Rose, M.; Hempel, S.; Ettl, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.

Submitted to the Protein Sequence Database, October 1998

A/Reference number: 215380

A/Accession: T04626

A/Molecule type: DNA

A/Residues: 1-321 <BEV>

A/Cross-references: EMBL:AL021749

C/Experimental source: cultivar Columbia; BAC clone F2009

C/Genetics:

A/Map position: 4

A/Intons: 26/1; 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2; 238/3; 281/1

A/Note: F2009.240

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: phosphotransferase

F:7-279/Domains: protein kinase homology <KIN>

Query Match

Best Local Similarity 41.0%; Score 921; DB 2; Length 321;

Matches 173; Conservative 57; Mismatches 74; Indels 14; Gaps 3;

RESULT 15

C71405

Probable casein kinase I - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: Columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 22-Oct-2001

C:Accession: C71405

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dijk
P.; Medler, H.; Medler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgomech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalvatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A:Reference number: A71400; M01D:9812113

A:Accession: C71405

A:Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-457 <BEV>

A:Cross-references: GB:297336; NID:q2244788; PTD:e326884; PID:q2244791

C:Genetics:

A:Map position: 4COP9-4G3845

C:Superfamily: kinase-related transforming protein; protein kinase homology

F:13-285/Domain: protein kinase homology <KIN>

Query Match 40.8%; Score 918; DB 2; Length 457;

Best Local Similarity 44.6%; Pred. No. 7.2e-48;

Matches 189; Conservative 76; Mismatches 95; Indels 64; Gaps 10;

QY 39 MGNPFRVKKIGGNGELRLKNTNEYVAIKLEPIKSRAPOLHEVRYKOLGSAG 98
 DB 10 VIGGKFKRLKLGSGSGFGLYGINIQGEVAVKLEPVKTRHPOLYESKITWFL-QGG 68
 QY 99 EGLPQVYFFGPGCKRYNMAVELLGPSELEDFDCDRTFTKTVLMAIQLLSRMEYVHSK 158
 DB 69 TGVPHLKMFPVEGEYSQWVIDLGPSELEDFENCKRIFSLKSVMLADQLICREYVMSR 128
 QY 159 NLIYRDYKPENFL--IGROGKKEVHTITDFGLAKETIDPETKRIPIREHKSSTGTAR 216
 DB 129 GFLHRDIPDNFNLGGLRRANO---VYIIDYGLAKKYLQOTOKHIPRENKRLTGTAR 184
 QY 217 YMSINPHLGKESRRDDLEALGHMEVFLRGSIPMOGLKADTLKERYOKIGDTRNPTIE 276
 DB 185 YASVNHILGIEQSRDDLESLGYLMPFLRGSIPMOGLKAGTKKQKYDKISEKMLTSVE 244
 QY 277 ALCENPEEMATYLRVYRLDFEKPDEYELRFTLFTDLFEKKGVTDFDAYDWV----- 329
 DB 245 TLCKSYDSEFTSYFHCRLSRFEDKPDYSYLRRLFRDLFIREGYQLDYFDWTISKYPI 304
 QY 330 ---GRPIPTP-----VGSV-----HVDGASAITRES 353
 DB 305 GSSSRPRPTPRPALDPPPPRAERAEKPTVGQDLRGRTGALIEAFTRRNVSSOGALGDRSR 364
 QY 354 H-THRDSPSQOQPL-----RNOVYSTNGELNVDDPTGAHNAPIITA--HAEVEY 400
 DB 365 HRSDDLPSSAKYHESRNGSTSKRGYISTRGSSA-EPSNHSKLFSSGSHHATTOR 423
 QY 401 VEEA 404
 DB 424 VPQS 427

Search completed: August 17, 2002, 20:17:39
 Job time: 3184 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2002, 20:16:35 ; Search time 24.7 Seconds

(without alignments)
661.524 Million cell updates/sec

Title: US-09-765-068-2

Perfect score: 2248
Sequence: 1 MDHPSREKDERQRTKPMQA.....EAKCCCFKRRKRTAQRHK 422

Scoring table: BLOSUM62
Gapop .10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2248	100.0	422	KC11_HUMAN	Q9HCP0: homo sapien
2	1915	85.2	390	KC11_RAT	Q62761: rattus norv
3	1809	80.5	448	KC13_RAT	Q62763: rattus norv
4	1783.5	79.3	447	KC13_HUMAN	Q9Y6M4: homo sapien
5	1776.5	79.0	415	KC12_HUMAN	P78368: homo sapien
6	1755	78.1	414	KC12_RAT	Q62762: rattus norv
7	1313.5	58.4	276	KC13_BOVIN	P35509: bos taurus
8	946.5	42.1	416	KC1E_MOUSE	P99674: mus musculu
9	940.5	41.8	416	KC1E_MOUSE	Q9JMK2: mus musculu
10	937	41.7	415	KC1D_HUMAN	P48730: homo sapien
11	936	41.6	428	KC1D_RAT	Q06486: rattus norv
12	924	41.1	365	HHP1_SCHPO	P40235: schizosacch
13	924	41.1	439	KC13_SCHPO	Q74135: schizosacch
14	922.5	41.0	435	CK12_SCHPO	P40234: schizosacch
15	917	40.8	446	CK11_SCHPO	P40233: schizosacch
16	907.5	40.4	400	HHP2_SCHPO	P40236: schizosacch
17	886.5	39.9	535	PAG8_KULTA	P40220: kluyveromyc
18	887.5	39.5	387	KC1D_ARATH	P42138: arabidopsid
19	885.5	39.4	546	CK12_YEAST	P23292: saccharomyc
20	884	39.3	538	DCO1_DROME	O76324: drosophila
21	877	39.0	532	CK11_YEAST	P23291: saccharomyc
22	867	38.6	578	YMR1_CAEEL	Q20471: caenorhabd
23	863.5	38.4	325	KC1A_RAT	P97633: rattus norv
24	862.5	38.4	325	KC1A_BOVIN	P35506: bos taurus
25	861.5	38.4	337	KC1A_CHICK	P71065: gallus gall
26	861.5	38.3	324	KC1A_PLAIF4	O15726: plasmodium
27	861.5	38.3	337	KC1A_HUMAN	P48729: homo sapien
28	860.5	38.3	434	HR25_YEAST	P99295: saccharomyc
29	820.5	36.5	337	KC1A_DROME	P54367: drosophila
30	816	36.3	341	TKL1_CAEEL	P42168: caenorhabd
31	800	35.6	524	CK13_YEAST	P39962: saccharomyc
32	795.5	35.4	336	KC1B_BOVIN	P35507: bos taurus
33	352.5	15.7	125	KC1A_PIG	O19175: sus scrofa

34	310	13.8	346	1	YMX8_CAEEL	P34516: caenorhabd
35	277	12.3	81	1	KC1D_RABIT	P11123: oryctolagus
36	268	11.9	283	1	KRB2_VACC	P21098: vaccinia vi
37	267	11.9	283	1	KRB2_VACC	P24362: vaccinia vi
38	265	11.8	303	1	V212_FOWPV	Q9J523: fowlpox vir
39	264.5	11.8	300	1	KRB1_VACC	P16913: vaccinia vi
40	264.5	11.8	300	1	KRB1_VARY	P33800: variola vir
41	263.5	11.7	300	1	KRB1_VACC	P20505: vaccinia vi
42	246	10.9	292	1	V226_FOWPV	Q9J509: fowlpox vir
43	229.5	10.2	256	1	KQ11_CAEEL	Q09503: caenorhabd
44	224.5	10.0	363	1	TKL2_CAEEL	P42169: caenorhabd
45	223	9.9	337	1	KAPC_ASCSU	P49673: ascaris suu

ALIGNMENTS

RESULT	ID	Query Match	Length	ID	Description
1	KC11_HUMAN	100.0	422	KC11_HUMAN	Q9HCP0: homo sapien
AC	Q9HCP0: Q9HCP0	100.0	422	KC11_HUMAN	Q9HCP0: homo sapien
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Casein kinase I, gamma 1 isoform (EC 2.7.1.-) (CKI-gamma 1).				
GN	CSNK1G1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kusuda J., Hirai M., Osada N., Hashimoto K.;				
RT	"Cloning, expression analysis and chromosomal mapping of human casein				
RT	kinase I gamma 1 (CSNK1G1): identification of two types of cDNA				
RT	encoding the kinase protein associated with heterologous				
RT	carboxy-terminal sequences."				
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR				
CC	PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS				
CC	AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.				
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1L (SHOWN HERE) AND 1S; ARE				
CC	PRODUCED BY ALTERNATIVE SPLICING.				
CC	-1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	CASEIN KINASE I SUBFAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: AB042563; BAB17839.1; -				
CC	EMBL: AB042562; BAB17838.1; -				
CC	MIM: 606274; -				
CC	InterPro: IPR000719; Euk_pkinase.				
CC	InterPro: IPR002290; Ser_thr_pkinase.				
CC	InterPro: IPR001245; Tyr_pkinase.				
CC	Pfam: PF00069; pkinase.1.				
CC	SMART: SM00220; S_TKc.1.				
CC	SMART: SM00219; TYRc.1.				
CC	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.				
CC	PROSITE: PS00107; PROTEIN_KINASE_DOM.1.				
CC	PROSITE: PS00108; PROTEIN_KINASE_ST.1.				
CC	Transferrin; Serine/threonine-protein kinase; ATP-binding;				
CC	Multi-gene family; Phosphorylation; Alternative splicing.				
CC	DOMAIN 44 315				
CC	FT NP_BIND 50 58 ATP (BY SIMILARITY).				

FT BINDING 73 73 ATP (BY SIMILARITY).
 FT ACT_SITE 164 164 BY SIMILARITY.
 FT VARSPPLIC 370 422 VVSSGELNVDPTGASHNAPITAHAEVVEAKCCCF
 FT KRRKKTQORH -> SLRTYAHEHYDNNNAIMHNGST
 FT (IN ISOBORM 15).
 SQ SEQUENCE 422 AA: 48511 MW: 8875922349B97645 CRC64;

Query Match 100.0%; Score 2248; DB 1; Length 422;
 Best Local Similarity 100.0%; Pred. No. 8,7e-162;
 Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNFNRVGRKKGCGNGEGLRL 60
 DB 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNFNRVGRKKGCGNGEGLRL 60
 QY 61 GKNLTNEYVAIKLEPIKSRAPQLHEVRFYKQLSAGEGLPQVYVYFGPCGKYNAMVLEL 120
 DB 61 GKNLTNEYVAIKLEPIKSRAPQLHEVRFYKQLSAGEGLPQVYVYFGPCGKYNAMVLEL 120
 QY 121 LGPSLEDFDLCDFRTFTLKTVMIAIQLLSMEVYHSKNLYRDVKNPENFLIGRGNKE 180
 DB 121 LGPSLEDFDLCDFRTFTLKTVMIAIQLLSMEVYHSKNLYRDVKNPENFLIGRGNKE 180
 QY 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAHYMSINTHLGKEOSRRDDEALGHM 240
 DB 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAHYMSINTHLGKEOSRRDDEALGHM 240
 QY 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAVYLRVRLDFFE 300
 DB 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAVYLRVRLDFFE 300
 QY 301 KPDEYELRTFTDLEFEKKGTFDYAYDWVGRPIPTVGSVHVDSGASAITRESHTHRDP 360
 DB 301 KPDEYELRTFTDLEFEKKGTFDYAYDWVGRPIPTVGSVHVDSGASAITRESHTHRDP 360
 QY 361 SQOQPLRNQVVSSTNGELNVDPTGASHNAPITAHAEVVEAKCCCFKRRKKTQOR 420
 DB 361 SQOQPLRNQVVSSTNGELNVDPTGASHNAPITAHAEVVEAKCCCFKRRKKTQOR 420
 QY 421 HK 422
 DB 421 HK 422

RESULT 2

KC13_RAT STANDARD: PRT: 390 AA.
 AC Q62761;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Casein kinase I, gamma 1 isoform (EC 2.7.1.-) (CKI-gamma 1).
 GN CSNK1G1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=95279411; PubMed=7759525;
 RA Zhai L., Graves P.R., Robinson L.C., Italiano M., Culbertson M.R.,
 RA Rowles J., Cobb M.H., Depauli-Roach A.A., Roach P.J.;
 RT "Casein kinase I gamma subfamily. Molecular cloning, expression, and
 RT characterization of three mammalian isoforms and complementation of
 RT defects in the Saccharomyces cerevisiae YCK genes.";
 RL J. Biol. Chem. 270:12717-12724(1995).
 CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
 CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CASEIN KINASE I SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: U22296; AAC52200.1; -
 DR HSSP: Q06486; 1CKI.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 44 315 PROTEIN KINASE.
 FT NP_BIND 50 58 ATP (BY SIMILARITY).
 FT BINDING 73 73 ATP (BY SIMILARITY).
 FT ACT_SITE 164 164 BY SIMILARITY.
 SQ SEQUENCE 390 AA: 45126 MW: 889DBF5952D40762 CRC64;

Query Match 85.2%; Score 1915; DB 1; Length 390;
 Best Local Similarity 96.0%; Pred. No. 8,4e-137;
 Matches 359; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNFNRVGRKKGCGNGEGLRL 60
 DB 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNFNRVGRKKGCGNGEGLRL 60
 QY 61 GKNLTNEYVAIKLEPIKSRAPQLHEVRFYKQLSAGEGLPQVYVYFGPCGKYNAMVLEL 120
 DB 61 GKNLTNEYVAIKLEPIKSRAPQLHEVRFYKQLSAGEGLPQVYVYFGPCGKYNAMVLEL 120
 QY 121 LGPSLEDFDLCDFRTFTLKTVMIAIQLLSMEVYHSKNLYRDVKNPENFLIGRGNKE 180
 DB 121 LGPSLEDFDLCDFRTFTLKTVMIAIQLLSMEVYHSKNLYRDVKNPENFLIGRGNKE 180
 QY 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAHYMSINTHLGKEOSRRDDEALGHM 240
 DB 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAHYMSINTHLGKEOSRRDDEALGHM 240
 QY 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAVYLRVRLDFFE 300
 DB 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAVYLRVRLDFFE 300
 QY 301 KPDEYELRTFTDLEFEKKGTFDYAYDWVGRPIPTVGSVHVDSGASAITRESHTHRDP 360
 DB 301 KPDEYELRTFTDLEFEKKGTFDYAYDWVGRPIPTVGSVHVDSGASAITRESHTHRDP 360
 QY 361 SQOQPLRNQVVSST 374
 DB 361 SQOQPLRNQVVSST 374

RESULT 3

KC13_RAT STANDARD: PRT: 448 AA.
 AC Q62763;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Casein kinase I, gamma 3 isoform (EC 2.7.1.-) (CKI-gamma 3).
 GN CSNK1G3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=95279411; PubMed=7759525;
 RA Zhai L., Graves P.R., Robinson L.C., Italiano M., Culbertson M.R.,
 Rowles J., Cobb M.H., Depaoli-Roach A.A., Roach P.J.,
 "Casein kinase I gamma subfamily. Molecular cloning, expression, and
 characterization of three mammalian isoforms and complementation of
 defects in the Saccharomyces cerevisiae YCK genes.";
 RL J. Biol. Chem. 270:12717-12724(1995).
 CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS.
 CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: TESTIS, BRAIN, HEART, KIDNEY, LUNG, LIVER, AND
 CC MUSCLE.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CASEIN KINASE I SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U22321; AAC52202.1; -
 DR HSSP: P40233; ICSN.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 43 313 PROTEIN KINASE.
 FT NP_BIND 49 57 ATP (BY SIMILARITY).
 FT BINDING 72 72 ATP (BY SIMILARITY).
 FT ACT_SITE 162 162 BY SIMILARITY.
 SQ SEQUENCE 448 AA; 51428 MW; 6065DEC2D98B3087 CRC64;

Query Match 80.5%; Score 1809; DB 1; Length 448;
 Best local similarity 77.7%; Pred. No. 9.3e-129;
 Matches 351; Conservative 29; Mismatches 38; Indels 34; Gaps 8;

DB 298 EKPDYDYLRLFTDLFPKRYKMYEDYEDWIGKOLPTVGVAGVQDPALSS-NREHQRDK 356
 |||||
 QY 360 -----PSQO---QPLRN-----QVSSVSTNGELVNDPTGAHSA 390
 |||
 DB 357 IQOSKQSDADHRAAMDSQANPHHLRAHLAADRGGSSVQVSSVSTNGELVNDPTGAHSA 416
 |||||
 QY 391 PITAAHEVEVEEAKKCCFFKRRKRTAORHK 422
 |||||
 DB 417 PITAPTEVEVDETKCCFFKRRKRTIORHK 448
 |||||
 RESULT 4
 KC13_HUMAN
 ID KC13_HUMAN STANDARD; PRT; 447 AA.
 AC Q9Y6M4; Q9Y6M3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Casein kinase I, gamma 3 isoform (EC 2.7.1.-) (CKI-gamma 3).
 GN CSNK1G3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=99126346; PubMed=9925945;
 RA Kusuda J., Hirai M., Toyoda A., Tanuma R., Hashimoto K.;
 "Cloning and chromosome mapping of the human casein kinase I gamma3
 gene (CSNK1G3).";
 RL Cytogenet. Cell Genet. 83:101-103(1998).
 CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS.
 CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 3 (SHOWN HERE) AND 3L/CSNK1G3L;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CASEIN KINASE I SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF049089; AAD26525.1; -
 DR EMBL: AF049090; AAD26526.1; -
 DR HSSP: P40233; ICSN.
 DR MIM: 604253; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Multigene family; Phosphorylation; Alternative splicing.
 FT DOMAIN 43 313 PROTEIN KINASE.
 FT NP_BIND 49 57 ATP (BY SIMILARITY).
 FT BINDING 72 72 ATP (BY SIMILARITY).
 FT ACT_SITE 162 162 BY SIMILARITY.
 FT VARSPLIC 430 430 K -> NCQKVLNM (IN ISOFORM 3L).
 SQ SEQUENCE 447 AA; 51501 MW; CFB9A16BF06BDC CRC64;

Query Match 79.3%; Score 1783.5; DB 1; Length 447;

Best Local Similarity 76.8%; Pred. No. 7.6e-127;
Matches 347; Conservative 30; Mismatches 40; Indels 35; Gaps 8;

```

QY 1 MDHSEKDER-QRTTRPMAORSAHCRSPSSSSSGVLMGPNFRVKGKIGCGNFGELR 59
  1 MENKKKDDKDDMAR-SGRSGHNRGTG-SSSSGVLWGPNFRVKGKIGCGNFGELR 58
QY 60 LGKMLTYNEVAIKLEPIKSRAPOLHLEFRYKOLGSGEGLPQVYFFGPCGYNAVLE 119
  59 LGKMLTYNEVAIKLEPIKSRAPOLHLEFRYKOLGSGEGLPQVYFFGPCGYNAVLE 117
QY 120 LLSGSELEPDLCDRTFLTKVLMIAIQLLSRMEYVHSHKLIYDVYPENFLIGROGKK 179
  118 LLSGSELEPDLCDRTFLTKVLMIAIQLLSRMEYVHSHKLIYDVYPENFLIGRPRKT 177
QY 180 EHVHIIDFGLAKETIDPETKKHPIYREHKSLGTGARMSINTHLGKQSRDLEALGH 239
  178 QOVHIIDFGLAKETIDPETKKHPIYREHKSLGTGARMSINTHLGKQSRDLEALGH 237
QY 240 MFMVFLRSLPFGKADTLKERYQIGDKRNTPIEALCENPEEMATYLRVYRDLDF 299
  238 MFMVFLRSLPFGKADTLKERYQIGDKRNTPIEALCENPEEMATYLRVYRDLDF 296
QY 300 EKPRYEYLRKFTLPEKKGTYEDYADWGRPIPTVGSYHVDGSAITRESHTHRD 359
  297 EKPRYEYLRKFTLPEKKGTYEDYADWGRPIPTVGSYHVDGSAITRESHTHRD 355
QY 360 PSQOO-----PLRN-----QVYSSTNGELNDVPTGASNA 390
  356 MOGSKNSADHRAAMDQANPHHLRAHLADRGGSGVQVYSSTNGELNDVPTGASNA 415
QY 391 PTAHAEEVEVEAKCCCFKRRKRTAQRHK 422
  416 PTAHAEEVEVEAKCCCFKRRKRTAQRHK 447

```

RESULT 5
KC12_HUMAN STANDARD; PRT; 415 AA.

AC P78368; 000704;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Casein kinase I, gamma 2 isoform (EC 2.7.1.-) (CKI-gamma 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=98066772; PubMed=9403068;
RA Kitabayashi A.N., Kusuda J., Hirai M., Hashimoto K.;
RT "Cloning and chromosomal mapping of human casein kinase I gamma 2
 (CSNK1G2)."
RL Genomics 46:133-137(1997).
RP SEQUENCE FROM N.A.
RA Lamerence J.E., McCreedy P.M., Skowronski E., Adamson A.M.,
 Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stiliwgen S.,
 Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
 Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 Liu S., Attix C., Andreise T., Tranheim R., Amico-Keller G.,
 Coffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 Kobayashi A., Olsen A.S., Carraro A.V.,
 Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases
 -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
 AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
 -1- SUBUNIT: MONOMER (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: Cytoplasmic.

```

CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U89896; AAB8627.1; -.
CC EMBL: AF001177; AAC00212.1; -.
CC EMBL: AC005306; AAC26983.1; -.
CC HSSP: 006486; 1CKI.
CC MIM: 602214; -.
CC InterPro: IPR007719; Euk-pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase.1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST.1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Multigene family; Phosphorylation.
CC DOMAIN
CC NP_BIND 52 60 ATP (BY SIMILARITY).
CC FT BIND 75 75 ATP (BY SIMILARITY).
CC FT ACT_SITE 165 165 BY SIMILARITY.
CC FT ACT_SITE 415 415 BY SIMILARITY.
CC SQ SEQUENCE 415 AA; 47457 MW; 036A39148A1DA038 CRC64;

```

Query Match 79.0%; Score 1776.5; DB 1; Length 415;
Best Local Similarity 80.0%; Pred. No. 2.3e-126;
Matches 333; Conservative 31; Mismatches 41; Indels 11; Gaps 3;

```

QY 7 EKDERQRTTKPMAORSAHCRSPSSSSSGVLMGPNFRVKGKIGCGNFGELR 66
  11 ETEGRRMSKAGGGRSSHGIRSSG--TSSGVLWGPNFRVKGKIGCGNFGELR 68
QY 67 NEVAIKLEPIKSRAPOLHLEFRYKOLGSGEGLPQVYFFGPCGYNAVLELGPSTLE 126
  69 NEVAIKLEPIKSRAPOLHLEFRYKOL-SATSEGVQVYFFGPCGYNAVLELGPSTLE 127
QY 127 DLFDLCRTFTLTKVLMIAIQLLSRMEYVHSHKLIYDVYPENFLIGROGKKEHYHII 186
  128 DLFDLCRTFTLTKVLMIAIQLLSRMEYVHSHKLIYDVYPENFLIGROGKKEHYHII 187
QY 187 DFLAKETIDPETKKHPIYREHKSLGTGARMSINTHLGKQSRDLEALGHMFTFLR 246
  188 DFLAKETIDPETKKHPIYREHKSLGTGARMSINTHLGKQSRDLEALGHMFTFLR 247
QY 247 GSILPFGKADTLKERYQIGDKRNTPIEALCENPEEMATYLRVYRDLDFEKPXYE 306
  248 GSILPFGKADTLKERYQIGDKRNTPIEALCENPEEMATYLRVYRDLDFEKPXYE 307
QY 307 LRTLFTLPEKKGTYEDYADWGRPIPTVGSYHVDGSAITRESHTHRDPSQOQPL 366
  308 LRTLFTLPEKKGTYEDYADWGRPIPTVGSYHVDGSAITRESHTHRDPSQOQPL 365
QY 367 RNQVYSSTNGELNDVPTGASNAPIPAHAEEVEVEAKCCCFKRRKRTAQRHK 422
  360 RNQVYSSTNGELNDVPTGASNAPIPAHAEEVEVEAKCCCFKRRKRTAQRHK 415

```

RESULT 6
KC12_RAT STANDARD; PRT; 414 AA.

AC Q62762;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Casein kinase I, gamma 2 isoform (EC 2.7.1.-) (CKI-gamma 2).
GN CSKRIG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=95279411; Pubmed=7759525;
RA Zhai L., Graves P.R., Robinson L.C., Italiano M., Culbertson M.R.,
RA Rowles J., Cobb M.H., Depauli-Roach A.A., Roach P.J.;
RA "Casein kinase I gamma subfamily. Molecular cloning, expression, and
RT characterization of three mammalian isoforms and complementation of
RT defects in the Saccharomyces cerevisiae YCK genes.";
RL J. Biol. Chem. 270:12717-12724(1995).
CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- PFM: AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: U22297; AAC52201.1; -.
DR HSSP: P40233; IC5N.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
KM Transferrase: Serine/threonine-protein kinase; ATP-binding;
KM Multigene family; Phosphorylation.
FT DOMAIN 46 315 PROTEIN KINASE.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
SQ SEQUENCE 414 AA; 47479 MW; 5445A740B48BD576 CRC64;

```

```

DB 247 GSLPWGIGKADTLKERYKIGDTRKRAPIEVLCSFPPEMATYLYRVRLDFFKPDYDY 306
QY 307 LRTFTDLFEKKGTTFDAXYMWGRPIPTPGSVYHVDGSAIIRHSTHRDRSQOQPL 366
DB 307 LRTFTDLFEKSGYVFDEYMWAGPLPTPIGVHPD-----VPSOPPHDK-AQLHT 358
QY 367 RNQVVSSTNGELANDDPTGAHSNAPITAAHEVEVEEAKCCFFKRRKKTAAQRK 422
DB 359 KNOALNSTNGELNTDDPTAGHSNAPIAPAEVADEKCCFFRRKRSLSQRK 414

RESULT 7
ID KC13_BOVIN STANDARD; PRT; 276 AA.
AC P35509;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Casein kinase I, gamma 3 isoform (EC 2.7.1.-) (CKI-gamma 3)
DE (Fragment).
GN CSKRIG3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92052129; Pubmed=1946367;
RA Rowles J., Slaughter C., Moornaw C., Hsu J., Cobb M.H.;
RA "Purification of casein kinase I and isolation of cDNAs encoding
RT multiple casein kinase I-like enzymes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9548-9552(1991).
CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: M76542; AAA30454.1; -.
DR HSSP: P40233; IC5N.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
KM Transferrase: Serine/threonine-protein kinase; ATP-binding;
KM Multigene family; Phosphorylation.
FT DOMAIN 29 >276 PROTEIN KINASE.
FT NP_BIND 35 43 ATP (BY SIMILARITY).
FT BINDING 58 58 ATP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.
FT NON_TER 276 276
SQ SEQUENCE 276 AA; 31510 MW; 69E9364A2E50C34C CRC64;

```

```

Query Match 78.1%; Score 1755; DB 1; Length 414;
Best Local Similarity 79.1%; Pred. No. 9.6e-125;
Matches 329; Conservative 33; Mismatches 42; Indels 12; Gaps 4;

```

```

Query Match 58.4%; Score 1313.5; DB 1; Length 276;
Best Local Similarity 91.3%; Pred. No. 8.7e-92;
Matches 253; Conservative 7; Mismatches 6; Indels 11; Gaps 3;

```



```

Db      180 ASINHHGITEOSRRDDLESGLGYLVNFIUNGLSIPMGKIAATNRQXYERISEKKMSTPLEV   239
               ||||| ||||| :||: || | ||||| : || : |||||
Oy      278 LCNPEEMATYLRIVRLDFFEKPDYEYLRTLPDLFEKKGYTDIAYDWGRPIPIPV   337
               ||: ||: |||| : ||: |||| || || || || ||: || ||
Db      240 LCKGPSEFSFYALNCRSLRFEDKDPDYSLROLFRNLFRHOGFSYXDYVDW-----   290
               ||: ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||
Oy      338 GSVHSDSAATIRSHTHRDSPSOQGQLRNQVYSTNGELAVDDPTGHSN   389
               :::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db      291 ---NMKGFAANRPEDVDREHERHERHEERMKGRLGSATRALPPGPPTGATAN   339
               ::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

RESULT
9
KCIE_MOUSE STANDARD: PRT; 416 AA.
AC QJUMK2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Casein kinase I, epsilon isoform (EC 2.7.1.1-) (CKI-epsilon).
GN CSNK1E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20106796; PubMed=10640823;
RA Kusuda J., Hirai M., Tanuma R., Hashimoto K.;
RT "cDNA cloning and chromosome mapping of the mouse casein kinase I
RT epsilon gene (Csnk1e)."
RL Cyogenet. Cell Genet. 87:99-101(1999).
CC -1 FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
CC -1 SUBUNIT: MONOMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1-1 PM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE SBR/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY. COULD BE THE ORTHOLOG OF DROSOPHILA
CC DOUBLE-TIME.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licenses@lsb-sib.ch).
CC -----
Cc      EMBL; AB028736; BAA88107.2; .
DR MGD; MG1:1351660; Csnk1e.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProSite; PS00107; PROTEIN_KINASE_ATP_1.
DR ProSite; PS00011; PROTEIN_KINASE_DOM_1.
DR ProSite; PS00108; PROTEIN_KINASE_ST_1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
RV Multigene family; Phosphorylation.
FT DOMAIN 9 277 PROTEIN KINASE.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 128 128 BY SIMILARITY.
FT ACT_SITE 416 AA; 47151 MW; 9561DF43BADA066 CRC64;
FT SEQUENCE

```

```

Query Match          41.8%   Score 940.5; DB 1; length 416;
Best Local Similarity 51.1%   Pred. NO. 1.6e-63;
Matches 180; Conservative 68; Mismatches 89; Indels 15; Gaps 3.

QY      38 LMVGNFRRVGKKIGCGNGELRLGKNLTINEVAIKLEPIKRAPOLHIEFYKQLSA 97
| | | : : : | | | : : : | : : : | | | | | : : : | | | : | | :

```

Dr 3 LRNVNKKYTLGKRRIGSGSGFDGYLLADINDSGEEVAIKLECVTKRHPOLHIESKFKMM-OG 61

Qy 98 GEGLPQVYVYFPCGKYNMAMVELLIGPSLEDFDLCDDRFETKTYLMIATOLLISREYHS 157

Db 62 GVGIPISIMWCAEGGYNYVMVELLIGPSLEDFNCSKRFSLKTYLLADQMSRIEYHS 121

Qy 158 KNLIIYRDVCPENFLIGROGNKKEHVIHIDEGLAKEYIDPEPKKHIPYREKHSILGTARY 217

Db 122 KNFIHRDVKPDPNFMGL--GKGNLYVIITIDGLAKKYADATHQIPIPERKNKILGTARY 179

Qy 218 MSINTHLKEOSRRDDELALGHMFYFLRGLIPMOGLKADTLKERYOKIGDTRKNTPIEA 277

Db 180 ASINTHLGIEGSRDDELSTGLYVLMFYENLGLSPMOGLKAATRKQYERISEKKNSTPIEV 239

Qy 278 LCENFPEEMATYTLKRYRLDFEPEKPDYIYLTPTDLEPEKGYFDYAYDVWGNRPIPIPV 337

Db 240 LCKGPFSEFSYFLNFCRSLRFPDVKPDYSYLRQLFRNLPHRQGSFSDYVFDW----- 290

Qy 338 GSVHVDGASVITRESHTHRDRPSQOCPLRNQVYSTNGELNVDPDPTGASHN 389

Db 291 ---NMLKFGAARNPEDVDRERRGHERERMQOLKGSATRALPPGPPGTATAN 339

RESULT 10

KCID_HUMAN

ID_KCID_HUMAN STANDARD; PRT: 415 AA.

AC P46730; Q9B7N5; 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Casein kinase I, delta isoform (EC 2.7.1.-) (CKI-delta).

GN CSNK1D.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid:9606; [1]

RN SEQUENCE FROM N.A.

RP TISSUE-Brain;

RC MEDLINE:96230338; PubMed:8786104;

RA Kusuda J., Hidari M., Hashimoto K.;

RT "Sequence analysis of the cDNA for the human casein kinase I delta (CSNK1D) gene and its chromosomal localization.";

RL Genomics 32:140-143(1996). [2]

RN SEQUENCE FROM N.A.

RP TISSUE-Choriocarcinoma;

RC Strausberg R.;

RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RL FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.

CC -1- ENZYME REGULATION: EXHIBITS SUBSTRATE-DEPENDENT HEPARIN ACTIVATION.

CC -1- SUBUNIT: MONOMER.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CASEIN KINASE I SUBFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_licensel@isb-sib.ch).

CC -----

CC EMBL; U29171; AAC50807.1; .

DR EMBL; U31285; AAC50808.1; .

DR EMBL; BC003558; AAH03558.1; .

DR HSSP; 006486; 1CKJ.

DR MIM; 600864; .

DR InterPro; IPR000719; Euk_Pkinase.

DR EMBL: U29171; AAC50807.1; -.
DR EMBL: U31285; AAC50808.1; -.
DR EMBL: BC003558; AAH03558.1; -.
DR HSSP: Q06486; 1CKJ.
DR MIM: 600864; -.
DR InterPro: IPR000719; Euk_Pkinase.

Db 347 TPTSHANTSPRVSQME-----REKVSMLHR 375

RESULT 12

HHPI_SCHPO STANDARD; PRT; 365 AA.

AC P40235;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Casein kinase I homolog hhpi (EC 2.7.1.-).

GN HHPI OR SPBC3H7.15.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

XX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SP66;

RX MEDLINE=94354807; PubMed=8074660;

RA Kearney P., Ebert M., Kuret J.;

RT "Molecular cloning and sequence analysis of two novel fission yeast

RT casein kinase-1 isoforms.";

RL Biochem. Biophys. Res. Commun. 203:231-236(1994).

RM [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=94298768; PubMed=8026462;

RA Dhillon N., Hoekstra M.F.;

RT "Characterization of two protein kinases from Schizosaccharomycetes

RT pombe involved in the regulation of DNA repair.";

RL EMBO J. 13:2777-2788(1994).

RM [3]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Lyne M., Rajandream M.A., Barrell B.G., Jimenez Martinez J.;

RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN DNA REPAIR. HAS A PROBABLE ROLE IN REPAIRING

CC ACTIVATED DNA AND MAY REGULATE THE ACTIVITY OF PROTEIN(S) INVOLVED

CC IN DOUBLE STRAND BREAK REPAIR CAUSED BY GAMMA RAYS.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CASEIN KINASE I SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL; U10863; AAA21544.1; -

DR EMBL; X78871; AAS54473.1; -

DR EMBL; AL031261; CAA20311.1; -

DR PIR; S44196; S44196.

DR HSPD; Q06486; ICKT.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; pkinase.1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.

KW transferase; Serine/threonine-protein kinase; ATP-binding; DNA repair;

KW Nuclear protein.

FT DOMAIN 11 279 PROTEIN KINASE.

FT NP_BIND 17 25 ATP (BY SIMILARITY).

FT BINDING 40 40 ATP (BY SIMILARITY).

FT ACT_SITE 130 130 BY SIMILARITY.

FT DOMAIN 289 323 GIN/PRO-RICH.

FT SEQUENCE 365 AA; 42450 MW; D637C950555F1339 CRC64;

Query Match 41.18; Score 924; DB 1; Length 365;

Best Local Similarity 49.28; Pred. No. 2,3e-62;

Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

QY 38 LMGPNFVGGKIGCGNGELRLGNLTNEVAIKLEPIRSAPOLHEFRYQOLGSA 97

DB 5 LRIQKRYIRIGRIKIGSGSFGDIYLTNVSGEVAIKLESTRKHPLEYERVYIL-SG 63

QY 98 GEGLPQVYFPGPCGKYNAMVELLGPSPLEDFDLCDRTFTTKTYLMAIQLSRMEYVHS 157

DB 64 GVGIFPVMFVEEDCYNNAMVDLSPSLDELFNPNRNRFSKTVLLADQLISREFIHS 123

QY 158 KNLIVRDYKPNFL-IGRGKKKEVHIIDFGLAKXYIDPEYKKAHPYREHKSITGTA 215

DB 124 KSPFHRDIPKPNFLMGIKRGNG---VNIDFGLAKYRDKHTLHIPYRENNKLTGTA 179

QY 216 RYMSINTHLGKQSRDLEALGHFMFPLGSLPWQGLKADTLKEROKIGDTNRNPI 275

DB 180 RYASINTHLGIEQSRDLESIGVLYFCRSLPWQGLKATYKOKYERIKERKISTPT 239

QY 276 EALCFNPEEMATYLRVYRRLDFEFKPDYEVYRLFTDLFEKGYTFPYADWVGRIPT 335

DB 240 EYLCGFPGFQESTYINTRSLRFDDKPDYATYLRKLFRLFCRQSYEPDYMDW----- 292

QY 336 PVGSVYVDSGASATRESHTHRDPSQO-----PLRN---QVSS 373

DB 293 -----TLKRTQODQHOQOLQQLSATFOAINPPERSFRNYOKRNPDE 338

QY 374 TNGELN-----VDDP--TGA-HSNAP 391

DB 339 KGDINTVTPVINDPSATGAQYINRP 364

RESULT 13

CKI3_SCHPO STANDARD; PRT; 439 AA.

ID C74135;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Casein kinase I homolog ck13 (EC 2.7.1.-).

DE CKI3 OR SPAC1805.05.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

XX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98322261; PubMed=9651503;

RA Kitamura K., Yamashita I.;

RT "Identification of a novel casein kinase-1 homolog in fission yeast

RT Schizosaccharomycetes pombe.";

RL Gene 214:131-137(1998).

RM [2]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;

RL Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR

CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS

CC AS SUBSTRATES.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CASEIN KINASE I SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL: AB010643; BAA32482.1; -
 DR EMBL: AL117390; CAB5846.1; -
 DR HSSP: P40233; ICSN.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_chir_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 15 286 PROTEIN KINASE.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 134 134 BY SIMILARITY.
 FT DOMAIN 376 382 POLY-GLN.
 FT DOMAIN 387 392 POLY-GLN.
 SO SEQUENCE 439 AA; 50215 MM; CE6A1B1C1A8A8F6 CMC64;

Query Match 41.1%; Score 924; DB 1; Length 439;
 Best Local Similarity 46.1%; Pred. No. 3e-62;
 Matches 196; Conservative 63; Mismatches 126; Indels 40; Gaps 6;

QY 31 SSSSSGVLMGPNFRVKGKICGNGELRLKNTNYVAIKLEPIKSRAPQHLERYF 90
 2 STTSHSVGVVHYRVGKIKIGSGFMFGVNLINNPALKEFSRSEVPOLRDEYLT 61
 QY 91 YKOGSAGEGLPOVYFGPGKYNAMVLELLGPSLEDFDCDRFTLTQVLMIAIOLLS 150
 62 YKLMGL-PGIPSVYYIGGEMNMLVMDLGPSEDFDYCGRRFSKTYAMAKQHT 120
 QY 151 RMEVYHKNLIRVDKRNFLIGROGKKEHVIHIDFLAKKEYIDPEKTHIPYREHS 210
 121 RIQSVHERHFIYRDIKPDNFIIGPGSKTENVIYAVDGMKQYRDXPHVHPYNEKS 180
 QY 211 LTGARFVSTHILGKESRDLLEALGHMVFYLRGSLPMOGLKADTLKRYOKIGDTK 270
 181 LSGTARFVSTHILGKESRDLLESMGHMVFYLRGSLPMOGLKAAKNKQYKIGTK 240
 QY 271 RNTGTEALCENPEPMATYLRVRLDFEEDKDEYELRTLTDFEKKGYEDVAYDMV- 329
 241 QVTLKELCEGYKPEFLQYMIYARNLGEAPDYLRSLDSLLKRLNETDDGKYDWT 300
 QY 330 ---GRPIPTPVGSYVH-----DSGASAITRESHTHD---RSGOQPLRNOVSS 373
 301 LNMCKGMQYSAKHVVQRHHTQGTNNRQSTIPYARTRONLLSPSKQTPVNNVVDAS 360
 QY 374 T-----NGELNVDDPTGAHSNAPITAH-AEVEVVEAKCCCFK 411
 361 VATQKDGIPKKAASPOVQOQOQTSSAQOQOPQVVEOPAPOTPTOPVDTQQAAPAPSE 420
 QY 412 KRKK 416
 Db 421 KSRK 425

RESULT 14
 CK12_SCHPO STANDARD; PRT; 435 AA.
 AC P40234; O9P798;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Casein kinase I homolog ck12 (EC 2.7.1.-).
 OS CK12 OR SPB35G2.05C.
 GN Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-SP66;
 RA MEDLINE-94216312; PubMed-8163505;
 RA Wang P.-C., Vancura A., Desai A., Carmel G., Kuret J.;
 RT "Cytoplasmic forms of fission yeast casein kinase-1 associate
 primarily with the particulate fraction of the cell.";
 RL J. Biol. Chem. 269:12014-12023(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.,
 RA Mccombe W.R.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
 CC AS SUBSTRATES. CK12 MAY CONTRIBUTE TO THE REGULATION OF
 CC MORPHOLOGY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CASEIN KINASE I SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: D06930; AAA19020.1; -
 DR EMBL: AL163702; CAB87367.1; -
 DR HSSP: P40233; ICSN.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_chir_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYTKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 12 282 PROTEIN KINASE.
 FT NP_BIND 18 26 ATP (BY SIMILARITY).
 FT BINDING 41 41 ATP (BY SIMILARITY).
 FT ACT_SITE 131 131 BY SIMILARITY.
 FT CONFLICT 169 169 H -> Y (IN REF. 1).
 SO SEQUENCE 435 AA; 49746 MM; 74CA7F1001B31F34 CRC64;

Query Match 41.0%; Score 922.5; DB 1; Length 435;
 Best Local Similarity 58.2%; Pred. No. 3.e-62;
 Matches 173; Conservative 53; Mismatches 68; Indels 3; Gaps 2;

QY 34 SSSVLMGPNFRVKGKICGNGELRLKNTNYVAIKLEPIKSRAPQHLERYF 93
 2 NSQTSVGVVHYRVGKIKIGSGFVIFGDMNLNOLAIKPEKSEPOLRDEYRTKL 61
 QY 94 L-GSAGEGLPOVYFGPGKYNAMVLELLGPSLEDFDCDRFTLTQVLMIAIOLLSRM 152
 62 LVGNA--GIPVYVYFGGGLNLIIVIDLGSLEDFEWCGRRRSVTVAMTAQMLSRV 119
 QY 153 EYVHKNLIRVDKRNFLIGROGKKEHVIHIDFLAKKEYIDPEKTHIPYREHS 212
 120 QTIHEKNLIVYDIDKPDNFIIGPSSRRNANVMYVDFGAKYRDPKTHOHPYSEKSL 179
 QY 213 GTARYMSTHILGKESRDLLEALGHMVFYLRGSLPMOGLKADTLKERYOKIGDKN 272
 180 GTARYMSTHILGKESRDLLEALGHMVFYLRGSLPMOGLKAAKNKHYKIKSEKQS 239
 QY 273 TPBALCENPEPMATYLRVRLDFEEDKDEYELRTLTDFEKKGYEDVAYDMV 329
 240 TSISELCAGFPNERSKMTYVRSLEFDEPDAFLQELFDVLANADNDINDGYVDM 296

```

RESULT 15
CKII_SCHPO STANDARD: PRT: 446 AA.
ID CKII_SCHPO
AC P40233; Q9UDU9;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Casein kinase I homolog ckl1 (EC 2.7.1.1).
GN CKII OR SPBC1347.06C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP66;
RX MEDLINE=94216312; Pubmed=8163505;
RA Wang P.-C., Vancura A., Desai A., Carmel G., Kuret J.;
RT "Cytoplasmic forms of fission yeast casein kinase-1 associate
RT primarily with the particulate fraction of the cell.";
RL J. Biol. Chem. 269:12014-12023(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-298.
RA MEDLINE=95196745; Pubmed=7889332;
RA Xu R.-M., Carmel G., Sweet R.M., Kuret J., Cheng X.;
RT "Crystal structure of casein kinase-1, a phosphate-directed protein
RT kinase.";
RL EMOB J. 14:1015-1023(1995).
CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
CC AS SUBSTRATES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce)
CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL; U06929; AAA19019.1; -.
DR EMBL; AL035548; CAB37437.1; -.
DR PDB; 1CSN; 08-MAR-96.
DR PDB; 2CSN; 31-JUL-95.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002290; Ser_thr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein Kinase; ATP-binding;
KW 3D-structure.
FT DOMAIN 12 274 PROTEIN KINASE.
FT NP_BIND 18 26 ATP.
FT BINDING 41 41 ATP.
FT ACT_SITE 131 131
FT CONFLICT 82 82 I -> V (IN REF. 1).
FT CONFLICT 310 310 R -> Q (IN REF. 1).
SQ SEQUENCE 446 AA; 50424 MW; D813483056CD8FDB CRC64;

```

Matches	188:	Conservative	69:	Mismatches	102:	Indels	54:	Gaps	9:
QY	39	MYGNPFVWGKKIGCGNFGELRLGKLNLYNEVAIKLEPKSAPQIHLHREPRYKQLSAG	98						
Db	7	YVGVHAYKVGRRIGEGSGFVIFEGTILNNQOVAIKFEPRSDAPOLADEYRFTYKLAGC	65						
QY	99	ESLPQVYVIFGCGKINAMVLELLGFSLEDFDLCDRTFTPLKTVLMAIOLSRMEVHSHK	158						
Db	66	TGIPNVYVFGQGLNIHLIVIDLGLSLEDLDLDCGRKFSVKTVAAMAQMLARVOSIHEK	125						
QY	159	NLIYDVKRPENFLIRGQKKKEHVHIIDFGLAKETIDETKHHIPYREHKSILTGARAYM	218						
Db	126	SLVYVDIRPDNLIGRPNKSNANMIVYDFGAWKFFRDVETKOHIPYREKNNLSGTARYM	185						
QY	219	SLNTHLGKQSRDLDLEAGHMFVETLSBMOGKAPTLKERQYKIDTTRNPIEAL	278						
Db	186	SINTHLGRQSRDLDLEAGHVMFVFLRGSLSWOGKAATYNOKEREIDEKKOSTPLREL	245						
QY	279	CENPDEEAMTYLRVYRLDFEFKKPDEYVYRTLTDFTEFKGTFDVAAYM	328						
Db	246	CAGPFEFEYKYMHVYKNALEFATPPDDYVQGLFSKYLELNTTEDENFDMNLNNGSGWO	305						
QY	329	-----VGRPIPTVGSVHVDGSAITPRESHNR-----DRP-----	360						
Db	306	SLKSRNALETENORSSKP-PAP------KLEKSPALONHAATQNVYKSRDYEKPRFAPHLM	360						
QY	361	---SQQOPLRNOV---VSTNGELNVDPDTGAHSN--APITAN--AEVEVEE 403							
Db	361	SASDSEAPRQNSLNPNPPTTKATTIVYPRDSGLATONAPRAVDVNDHDSSEKVTNE 413							

Search completed: August 17, 2002, 20:23:54
Job time: 439 sec

Query Match	40.88;	Score 917;	DB 1;	Length 446;
Best Local Similarity	45.58;	Pred. No. 1e-61;		

```

Oy 67 NEVYAIKLEPIKSRAPOLHLEYRYKOLGSAG-----EG 100
Db 69 NEVYAIKLEPIKSRAPOLHLEYRYKOLSTGEADSGTGPALLGOOMLRTSPMDVSFAEG 128
Oy 101 LPQVYFPGPCGKYNMVLELLGSLLEDFLDCDRTFTLKTVMIAIQLLSRMEYVSKNL 160
Db 129 VPQVYFPGCGKYNMVLELLGSLLEDFLDCDRTFTLKTVMIAIQLLIRMEYVHTKSL 188
Oy 161 IYRDVKNPFLRGOGKKNKKNHIIIDGLAKEXIDPEKTKIIPREKHSLSGTARYMSI 220
Db 189 IYRDVKNPFLRGOGKKNKKNHIIIDGLAKEXIDPEKTKIIPREKHSLSGTARYMSI 248
Oy 221 NTHLKEOSRRDLDLALGHMFYFLRSGSLPMOGLKADTLKEXYKIGDKRATPEALCE 280
Db 249 NTHLKEOSRRDLDLALGHMFYFLRSGSLPMOGLKADTLKEXYKIGDKRATPEALCE 308
Oy 281 NFPEEMATYLRVYRLDFFEKPDYELRTLTDFEKKGYTFDYAVDWYGRDIPPPVGSV 340
Db 309 SPPEEMATYLRVYRLDFFEKPDYELRTLTDFEKKGYTFDYAVDWYGRDIPPPVGSV 368
Oy 341 HVDASASATRESHTHRDRPSQOOLRNQVYSTNGELNVDPGTGASHNAPTITAAVEYV 400
Db 369 HPD-----VPSQPHRDK--AQLHTKNQALNSTNGELNVDPGTGASHNAPTITAAVEYV 420
Oy 401 VEEAKCCCFEKKRKRKKTQRHK 422
Db 421 ADETKCCCFEKKRKRKKSJORHK 442

RESULT 2
O96AE9 PRELIMINARY: PRT: 307 AA.
ID O96AE9.
DC O96AE9.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE; AND RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017236; AAH17236.1; -.
KM KINASE.
SQ SEQUENCE 307 AA; 35701 MW; 9CA5DD47CB473186 CRC64;

Query Match 72.6%; Score 1632; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 4,6e-134;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 241 HVDASASATRESHTHRDRPSQOOLRNQVYSTNGELNVDPGTGASHNAPTITAAVEYV 300
Oy 416 KTAORHK 422
Db 301 KTAORHK 307

RESULT 3
O9VEX2 PRELIMINARY: PRT: 422 AA.
ID O9VEX2.
DC O9VEX2.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE CG6963 PROTEIN.
CN GISH OR CG6963.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe C.R., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bens P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Broxstein P., Brotter P.,
RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weissbrock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh K.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB007712; AAF5293.1; -.
DR HSSP; Q06486; ICK1.
DR Flybase; FBgn0011253; gish.
DR InterPro; IPR000719; Ser_thr_kinase.
DR InterPro; IPR002290; Euk_thr_kinase.
DR Pfam; PF00069; pkinase.1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.

```


DR PROSITE: PS00108: PROTEIN_KINASE_ST. 1.
 KM ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 422 AA; 48183 MW; 41DA2B7AB/3DDBOF CRC64;

Query Match 69.1%; Score 1553; DB 5; Length 422;

Best Local Similarity 70.8%; Pred. No. 5,6e-127;
 Matches 294; Conservative 41; Mismatches 52; Indels 28; Gaps 4;

```

OY 32 SSSGVLNVPNFRVGRKKIGCGNFGEELRGKNTYNEVVAIKLEPIKSRAPQLHEERY 91
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 9 STTGVLNVPNFRVGRKKIGCGNFGEELRGKNTYNEVVAIKLEPIKSRAPQLHEERY 68
OY 92 KDLGSGDELPDYVYFGPGCKYNAVLELSPLEDPDLCDRTFTLKVMAIQLSR 151
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 69 KILGSAEGVPDYVYFGPGCKYNAVLELSPLEDPDLCDRTFTLKVMAIQLSR 128
OY 152 MEVYHSKNLYDVPENFLIGROGKKEVHIIDFLAKERYIDPEPKKHIPREHSL 211
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 129 IEVYHSKNLYDVPENFLIGROGKKEVHIIDFLAKERYIDPEPKKHIPREHSL 188
OY 212 TGTARYMSINTHLGKQSRDDEALGHNMFYFLRGSLEPMOGLKADTLKERYOKIGDTR 271
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 189 TGTARYMSINTHLGKQSRDDEALGHNMFYFLRGSLEPMOGLKADTLKERYOKIGDTR 248
OY 272 NPIPEALCENFEPEMATYLRVRRLDPEKPDYELRTLTDLFEKKGYTPYADWGR 331
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 249 AAPIELCDGHEEFAVYLRVRRLDPEKPDYELRTLTDLFEKKGYTPYADWGR 308
OY 332 PAPTGVSVHVDGSAI---TRESH-----THDRPSQOQPLRN----- 368
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 309 TMSITPGS--LDTGHEVITSPKDKRHNVTAKTNAGGVAAWDVCRPGATLGNLTPADRH 366
OY 369 ---QVVSSTNGELNVDPTGAHNAPIATAHAEVVEAEKCCCFKKRKKTAQR 420
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 367 GSVQVVSSTNGELNVDPTGAHNAPIATAHAEVVEAEKCCCFKKRKKTAQR 421

RESULT 4
OY9H5M4 PRELIMINARY; PRT; 280 AA.
AC OY9H5M4;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CDNA: FLJ23304 FIS, CLONE HEP11377.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Iisaga T., Sugano S.;
RT "NEBO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSSP; 006486; 1CKJ.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase.1.
DR SMART; SM00220; S_TKc.1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM.1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 280 AA; 32665 MW; 59DEIF509/8039CD CRC64;

```

Query Match 66.4%; Score 1492; DB 4; Length 280;
 Best Local Similarity 99.6%; Pred. No. 6,3e-123;
 Matches 279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 143 MIAIQLLSRMEVYHSKNLYRDVKNPENFLIGROGKKEVHIIDFLAKERYIDPEPKK 202
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1 MIAIQLLSRMEVYHSKNLYRDVKNPENFLIGROGKKEVHIIDFLAKERYIDPEPKK 60
OY 203 IPYRHKSLTGTARYMSINTHLGKQSRDDEALGHNMFYFLRGSLEPMOGLKADTLKER 262
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 61 IPYRHKSLTGTARYMSINTHLGKQSRDDEALGHNMFYFLRGSLEPMOGLKADTLKER 120
OY 263 YOKIGDTKRNPIEALCENFEPEMATYLRVRRLDPEKPDYELRTLTDLFEKKGYTF 322
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 121 YOKIGDTKRNPIEALCENFEPEMATYLRVRRLDPEKPDYELRTLTDLFEKKGYTF 180
OY 323 DYAYWVGSRPTTPVGSVHVDGSAITRESHTHDRPSQOQPLRNQVVSSTNGELNVD 382
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 181 DYAYWVGSRPTTPVGSVHVDGSAITRESHTHDRPSQOQPLRNQVVSSTNGELNVD 240
OY 383 PTGAHNAPIATAHAEVVEAEKCCCFKKRKKTAQRHK 422
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 241 PTGAHNAPIATAHAEVVEAEKCCCFKKRKKTAQRHK 280

RESULT 5
OY9J76 PRELIMINARY; PRT; 416 AA.
AC OY9J76;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CASEIN KINASE 1 EPSILON.
DE RCKLE.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Takano A., Shimizu K., Kani S., Buils R.M., Okada M., Nagai K.;
RT "Cloning and characterization of rat casein kinase 1 e.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB042191; BAB03472.1.
DR HSSP; 006486; 1CKJ.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase.1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM.1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 416 AA; 47292 MW; 38D94/95AE854486 CRC64;

```

Query Match 42.2%; Score 948.5; DB 11; Length 416;
 Best Local Similarity 47.6%; Pred. No. 2,7e-74;
 Matches 188; Conservative 75; Mismatches 107; Indels 25; Gaps 5;

```

OY 38 LMGVGNFRVGRKKIGCGNFGEELRGKNTYNEVVAIKLEPIKSRAPQLHEERYQOLGSA 97
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 3 LMGVGNFRVGRKKIGCGNFGEELRGKNTYNEVVAIKLEPIKSRAPQLHEERYQOLGSA 61
OY 98 GEGDLPDYVYFGPGCKYNAVLELSPLEDPDLCDRTFTLKVMAIQLSRMEYVHS 157
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 62 GVGISIRKMGCEGEGYVNMVVELLPSPLEDPDLCDRTFTLKVMAIQLSRMEYVHS 121
OY 158 KNLVYRDVKNPENFLIGROGKKEVHIIDFLAKERYIDPEPKKHIPREHSLGTARY 217
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 122 KNLVYRDVKNPENFLIGROGKKEVHIIDFLAKERYIDPEPKKHIPREHSLGTARY 179
OY 218 MSINTHLGKQSRDDEALGHNMFYFLRGSLEPMOGLKADTLKERYOKIGDTRNTPIEA 277
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 180 ASINTHLGKQSRDDEALGHNMFYFLRGSLEPMOGLKADTLKERYOKIGDTRNTPIEV 239

```

```

0Y 218 LCEANPEEMATLYKRVRLDFFEEKPPDYEYLTFTDLEFEEKGYTFDYADVMGNPIPTPV 333
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 LCKGYPSEFSEYTLNFCRSLRFDDEDDPSYLRQLFRNLFRHSGFSYDVFYDM----- 290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 338 GSYHVDASASLITESHHRHRRPQOQPLRNQVYSSINGELNVDDPFGAHSN-----API 392
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 ---NMLKGAARNPEDEDYDEREREREREREMQLGSASTRALPGPPTGATANRLRSAAP 347
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 393 TAAHAEVEVEEA-----KCCCFKRRKRRKKTQAORHK 422
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 VASTPASRIQAGNTSPRAISRADRRERVSRLRLR 382
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT	6			
09UKDO				
ID	09UKDO	PRELIMINARY:	PRT:	416 AA.
AC	Q9UKD0			
DT	01-OCT-2000 (TREMBLrel, 15, Created)			
DT	01-OCT-2000 (TREMBLrel, 15, Last annotation update)			
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)			
DE	CASEIN KINASE I EPSILON.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20237939; PubMed=10775102;			
RA	Lowrey P.L., Shimomura K., Antoch M.P., Yamazaki S., Zemenides P.D.,			
RA	Ralph M.R., Menaker M., Takahashi J.S.;			
RT	"Positional syntenic cloning and functional characterization of the			
RL	mammalian circadian mutation tau.";			
CC	Science 288:483-492(2000).			
CC	1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL: AF423236; AAF65549.1; -.			
DR	HSSP: Q06486; 1CKT.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_pkinase.			
DR	Pfam: PFO0069; pkinase; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_SF; 1.			
DR	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
FT	SEQUENCE 416 AA; 38BD4799AE339E86 CRC64;			
FT	VARNAME 178 I/8 R -> C.			

[illegible]

```

OY      338 GSVHVDSSA:ITRESHTHRDRP:SOQD:LNQVYSS:STNGEL:VNDP:GTASN:-----AP: 3922
Db      231 ---NMLTKG:ARNP:EDVD:RER:REHER:EREMQ:LG:SATRAL:PP:PP:GTAT:NR:LSA:AP 347
OY      393 TAAAEVEVEEA:---KCCCFK:RRKRRK:TAQRHK 422
Db      348 VASTPASH:RIQAGNTSP:PAISR:ADREKRV:SR:RLR 382

```

Q99PS2	7	PRELIMINARY;	PRT;	506 AA.
AC	Q99PS2;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	CASEIN KINASEI EPISTON.2.			
GN	CKIE-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Takano A., Nagai K.;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-203593300; PubMed-10899319;			
RA	Takano A., Shimizu K., Kani S., Buhrs R.M., Okada M., Nagai K.;			
RT	"Cloning and characterization of rat casein kinaseI."			
RL	FEMS Lett. 477:106-112(2000).			
CC	1-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL; AB056113; BAB32922.1; -.			
DR	HSSP; Q06486; ICKU.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_kinase.			
DR	InterPro: IPR001245; Tyr_kinase.			
DR	pfam; PF00069; pkinase.1.			
DR	SMART; SM00220; S_TKC; 1.			
DR	SMART; SM00219; TYRC; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_AFP; 1.			
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_SF; 1.			
KW	ATP-Binding; Kinase; Serine/threonine-protein kinase; Transferase.			
QW	SEQUENCE 506 AA; 56923 MW; 9DF11C50CEA96898 CRC4;			

	Query Match	42.2%	Score 948.5;	DB 11;	Length 506;
	Best Local Similarity	47.6%,	Pred. No. 3.5e-74;		
	Matches 188;	Conservative 75;	Mismatches 107;	Indels 25;	Gaps 5;
Qy	38 LAMVGNEFRVAGKIGGNGNELRLGNLTNTXEVAKLEPIKRAPOLHEVFYKOLGSA	97			
	: : : : : : : : : : : : : : : :				
Db	3 LRVGKRYLGRKIRISGSFGDIYLCANINISGEVAIKLECCKTKHQLIESEFFYMM-QG	61			
Qy	98 GEGELPYYVFPFCPCGRKYNNAMVELLPSSLEDLFEDLCDRFETTLKTVMIAIQLLSMEYVS	157			
	: : : : : : : : : : : : : : : :				
Db	62 GVGIPTSIWCAEGBGVNWNMELLSPSLEDLFENFSRSFSLKTVLLADQMISREYIHS	121			
Qy	158 KNLIIYRDVKPENFELIGROGNKEHYIHIDPLAKEYIDPETKKHIIPYRHKSLTGVIARY	217			
	: : : : : : : : : : : : : : : :				
Db	122 KNFIHRDVKPNDFLMGL--GKKGNLYIIDFLAKKYDARTHOHIPPKNKNLTGTARIY	179			
Qy	218 MSINTHGKEOSRRDDLEALGHMFYFLRSGSLPMOGLRADPLKEKYOIGDKRTPTLEA	277			
	: : : : : : : : :				
Db	180 ASINTHLGIESRRDLESILYLVMTYFMUGSLPMDGLAAARKQRYERIISEKKNSTPREV	239			
Qy	278 LCENEPEEMAYLRVRRLDPFEFKDEYEYLKRLFTEDLPEKKGYFDVYDWGVRIPVPV	337			
	: : : : : : : : : : : : : : : :				
Db	240 LCKGYPSESFSTYLNCRSLRFDRDKPDYITYLQOLFNLHHRGOFSTIDYFDM-----	290			
Qy	338 GSIVHSDCASATIRSRSHHRDRPSGOQDELRAQOVYSTINGELINVDDPTGAHSN----	API 392			

```
Db 291 ---NMKFGAARNPEVDREPEREREERMGQLGSAITRALPPEPTIGATNRLSAAP 347
QY 393 TAAAEVEVEEA---KCCCFEKKRKKTAQRHK 422
Db 348 VASPPASRIQOAGNTSPRAISRADREKRVSWRLHR 382

RESULT 8
Q9PU12 PRELIMINARY; PRT; 416 AA.
AC 09PU12;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CASEIN KINASE I EPSILON.
GN CKE.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9445220; PubMed=10517632;
RA Peters J.M., McKay R.M., McKay J.P., Graff J.M.;
RT "Casein kinase I transduces wnt signals.";
RL Nature 401:345-350(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF183394; AAF01032.1; -.
DR HSP; Q06486; ICKI.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
KW KM
SQ SEQUENCE 416 AA; 47315 MW; F0F7CB691A4F4CDF CRC64;

Query Match 42.1%; Score 945.5; DB 13; Length 416;
Best Local Similarity 52.2%; Pred. No. 4.8e-74;
Matches 186; Conservative 62; Mismatches 85; Indels 23; Gaps 6;

QY 38 LAMGPNFVGGKKGNGNELRLGKNLYTNEVAIKLEPIKSRAPOLHLEVFYKQLGSA 97
Db 3 LRVGNKYLGRKIGSGSGDIYLGANITATGEVAIKLECVTKHPOLHIESKFKMM-QG 61
QY 98 GEGLPQVYTFPGCKRYNMAVLELGPSELDLPDLCDRTFTLTKTYLMAIAIQLSRMEYHS 157
Db 62 GVGIPISIMWCAEGDYNNVMVLELGPSELDLPDLCDRTFTLTKTYLMAIAIQLSRMEYHS 121
QY 158 KNLIVDVKPNFNLIGRGNKKKEHYIHIDFLAKKEYIDPETKKHIPPYREKSLTGTA 217
Db 122 KNFHRDVKPNFNLIGRGNKKKEHYIHIDFLAKKEYIDPETKKHIPPYREKSLTGTA 179
QY 218 MSINTHLGKEOSRRDLEALGHMFYFLRGSLLPMOGLKADTLKERYOKIGDTKRNTPIEA 277
Db 180 ASINTHLGIEOSRRDLEALGHMFYFLRGSLLPMOGLKAAKRRKYEISKSKMSTPIEV 239
QY 278 LCENFPEEMATYLRVRLDFEKKPDYEVYLTFTDLFEKKGYTFDYAVDWGRIPIPV 337
Db 240 LCKGVSFSTYLNFCRSLRFDDKFDYSYLRQLFENLHROGFSYDYVDM----- 290
QY 338 GSVHVDGASA-----ITRSHTHDRPSQOQPLRNQVVSSTNGELNVDPGASNS 389
Db 291 ---NMKFGAARNPEVDREPEREREERMGQLGSAITRALPPEPTIGATNRLSAAP 339

RESULT 9
Q9U8F8 PRELIMINARY; PRT; 330 AA.
```

```
AC Q9U8F8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CASEIN KINASE I HOMOLOG 2 (CASEIN KINASE 1.2).
GN CK1.2.
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y;
RA Spadafora C., Repetto Y., Robello C., Morello A., Gamarro F.,
RA Castanys S.;
RT "Trypanosoma cruzi casein kinase 1 gene homolog 2.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Spadafora C., Repetto Y., Robello C., Morello A., Castanys S.,
RA Gamarro F.;
RT "Trypanosoma cruzi casein kinase 1 homolog 2, complete mRNA
sequence.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF089709; AAF00025.1; -.
DR EMBL: AF274059; AAK58696.1; -.
DR HSP; Q06486; ICKI.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
KW KW
SQ SEQUENCE 330 AA; 38093 MW; C29B34775327E72E CRC64;

Query Match 41.9%; Score 942; DB 5; Length 330;
Best Local Similarity 53.3%; Pred. No. 7e-74;
Matches 178; Conservative 61; Mismatches 79; Indels 16; Gaps 4;

QY 38 LAMGPNFVGGKKGNGNELRLGKNLYTNEVAIKLEPIKSRAPOLHLEVFYKQLGSA 97
Db 5 LRVGNFRLGKIGSGSGEIFRGTNIOTGEVAIKLEQATRHPOALMLAEAFYRLNAG 64
QY 98 G--EGLPQVYTFPGCKRYNMAVLELGPSELDLPDLCDRTFTLTKTYLMAIAIQLSRMEY 155
Db 65 GGVGIPILFYGVEGEFNNVMVMDLGPSELDLPDLCDRTFTLTKTYLMAIAIQLSRMEY 124
QY 156 HSKNLIYDVKPNFNLIGRGNKKKEHYIHIDFLAKKEYIDPETKKHIPPYREKSLTGTA 215
Db 125 HSKSVIHRDVKPNFNLIGRGNKKKEHYIHIDFLAKKEYIDPETKKHIPPYREKSLTGTA 182
QY 216 RYMSINTHLGKEOSRRDLEALGHMFYFLRGSLLPMOGLKADTLKERYOKIGDTKRNTPI 275
Db 183 RYCSINTHLGIEOSRRDLEALGHMFYFLRGSLLPMOGLKADTLKERYOKIGDTKRNTPI 242
QY 276 EALCENFPEEMATYLRVRLDFEKKPDYEVYLTFTDLFEKKGYTFDYAVDWGRIPIPV 335
Db 243 ETLCKGFAEPAEAYLYNIRSLRFEDKPDYSYLRQLFRELFIREFGYHVDVDM----- 296
QY 336 PVGSHVDGASAITRSHTHDRPSQOQPLRNQ 369
Db 297 -LKRHHEN-----LKAEGSGOQEKQOQOQER 324

RESULT 10
Q9JUT5 PRELIMINARY; PRT; 367 AA.
AC Q9JUT5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
```

NN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.,
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBD databases.
 NN [2]

RESULT	12	
Q9FEH8		
ID	Q9FEH8	PRELIMINARY;
AC	Q9FEH8:	PRT: 476 AA.
DT	01-MAR-2001 (TReMBLrel, 16, Created)	
DT	01-MAR-2001 (TReMBLrel, 16, Last sequence update)	

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:21:26 ; Search time 1892.02 Seconds
(without alignments)
14035.673 Million cell updates/sec

Title: US-09-765-068-1

Perfect score: 1269
Sequence: 1 atggacatctagtagga.....ctgtcagcgccacagtga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_bhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description

SUMMARIES

1	1269	100.0	1269	6	AX202215	Sequence
2	1269	100.0	1269	6	AX250158	Sequence
3	1269	100.0	1649	9	AB042563	Homo sapi
4	1269	100.0	1968	6	AX202217	Sequence
5	1269	100.0	2066	9	BC017236	Homo sapi
6	1146.4	90.3	4417	6	AX239864	Sequence
7	1143.4	90.1	1377	6	AX239866	Sequence
8	979	87.7	1950	9	AB042562	Homo sapi
9	852.8	67.2	3552	9	RN022296	Sequence
10	608.8	48.0	2405	6	I73428	Sequence
11	603	47.5	1767	9	HS089896	Homo sapien
12	603	47.5	2446	9	BC020972	Homo sapi
13	577.6	45.5	1572	10	RN022297	Sequence
14	566.6	44.6	2547	10	RN022321	Sequence
15	564.8	44.5	1734.29	6	I73429	Sequence
16	561.8	44.3	2421	9	AF049089	Homo sapi
17	561.8	44.3	2453	9	AF049090	Homo sapi
18	548.8	43.2	2773	9	AF001177	Homo sapi
19	514.8	40.6	2363	10	BC004839	Mus muscu
20	470	37.0	1162	4	BOVCKIG	Bovine case
21	299.8	23.6	1541	8	AT048779	Arabidopsi
22	299.8	23.6	1939	8	AY065409	Arabidopsi
23	296.4	23.4	1632	8	SP006929	Schizosacch
24	293.4	23.1	2652	5	AF183394	Xenopus 1
25	292	23.0	1402	9	BC006490	Homo sapi
26	291.8	23.0	1229	10	AB042192	Rattus no
27	291.8	23.0	1251	10	AB042191	Rattus no
28	291.8	23.0	1329	8	AY074536	Arabidops
29	291.8	23.0	1331	9	HUMCSNK1E	Homo sapien
30	291.8	23.0	1374	8	AY060528	Arabidops
31	291.8	23.0	1374	8	AB024597	Homo sapi
32	291.8	23.0	1443	8	AY040071	Arabidops
33	291.8	23.0	1528	10	AB056113	Rattus no
34	291.8	23.0	1715	8	AF250343	Arabidops
35	291.8	23.0	1732	8	ATCKR11	Arabidops
36	291.8	23.0	1740	8	AY054179	Arabidops
37	291.8	23.0	1793	8	AY052364	Arabidops
38	291.8	23.0	2044	8	AF360257	Arabidops
39	291.8	23.0	2044	8	AF360257	Arabidops
40	291.6	23.0	1370	3	AF003547	Dictposte
41	288.8	22.8	1711.46	9	AL161450	Human DNA
42	287	22.6	1251	10	AF242536	Mesocricet
43	283.8	22.4	978	10	RN077582	Rattus norv
44	283.4	22.3	1900	6	AX280985	Sequence
45	282.8	22.3	1911	9	HS029171	Human case1

ALIGNMENTS

RESULT 1
AX202215
LOCUS AX202215 1269 bp DNA linear PART 30-AUG-2001
DEFINITION Sequence 1 from Patent WO0153493.
ACCESSION AX202215
VERSION AX202215.1 GI:15391999
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1269)
Donoho, G., Hilbun, E., Turner, C.A., Friedlich, G., Zambrowicz, B. and
Sands, A.T.
TITLE Human kinase protein and polynucleotides encoding the same
JOURNAL Patent: WO 0153493-A 1 26-JUL-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source 1. 1269
location/Qualifiers
1. 1269
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 390 a 284 c 297 g 298 t
ORIGIN

Query Match 100.0%; Score 1269; DB 6; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggaccatcctagtaggaagaagatgaaagacagacgacacaaacccaatgacaa 60
 Db 1 ATGACACATCTCTAGTAAAGAAAAGATGAAGAACACGACCAATCAACCATGGACAA 60

QY 61 aggaagtcacacgtctctgacacacatctgctccatcgtctctcttggtcttatgtg 120
 Db 61 AGGAGTCACACCTCTCTGACCAATGCTGCTCTCATGCTCTCTGGGGTCTTATGCTG 120

QY 121 ggaaccaactcaaggtctgcaagaagataagatgctggaacttcggaagctcagatta 180
 Db 121 GGACCCAACTTCAGAGGTTGGCAAGATAGATGTGGAACTTCGGAGACTCAGATTA 180

QY 181 ggtaaaaatctctacaccaaataatgtagcaatcaactggaaacaaataacacgt 240
 Db 181 GGTAAAAATCTCTACACCAATGAATATGTAGCAATCAAACTGAAACCAATTAACGT 240

QY 241 gttcccaagctctcttaagaagtagacaattatataacgtctggcagtgcgatgaagt 300
 Db 241 GCTCCACAGCTTCAATTAGAGTACAGATTTTATTAACAGCTTGGCAAGTGAAGGT 300

QY 301 ctcccaaggtgtagtaactcttgacacatgtggaataataatgcatgtgtcagatc 360
 Db 301 CTCGCCAGAGGTATTAATTGGACATGTGGAAATATATATGCGATGCTCTGGACTC 360

QY 361 ctggccctagcttggaagactgttgacactctgacacgaacattacttgaagacg 420
 Db 361 CTGGCCCTAGCTTGAGAGCTTGTGACTCTGTACCCCAACATTTACTTTGAAGACG 420

QY 421 gttcattatgtagacacacagctgctcttcgaaatggaatacgtgcactcaaaagactc 480
 Db 421 GTGTTATGATAGCCATCCAGCTGCTTTCGAAATGGAATGCGTCACTCAAAACACTC 480

QY 481 attaccgaagatgtcaagacgaagaactctctgtatgtgcagacgaagcaataagaag 540
 Db 481 ATTATACGAGATGTCAAGCCAGAACTCTCTGATGTGTGCAAGCAATTAAGAAAGAG 540

QY 541 catgtataacacattatagaactctggaactggcgaagaatacatgacccgaaacaa 600
 Db 541 CATGTTATACACATTATAGACTTTGGACTGGCCAAAGAAATCAATTGAACCCGAAACCAA 600

QY 601 aaacacactactatagaagaacaaagtttaactiggaactggaagaatataitctatc 660
 Db 601 AAACACATACCTTATAGGAAACAAAGTTTAATCTGAACTGCAAGATATATGTCTATC 660

QY 661 aacacgactctgcaagaagcaaacggaagatgatttgaagccctagagccatag 720
 Db 661 AACACGACTCTTGCAAAAGCAAAAGCCGAGATGATTTGGAAGCCCTAGAGCCATATG 720

QY 721 ttaatgatttctctcgaggcagctccctcgcaaggaactcaagcttgacacattaaa 780
 Db 721 TTATATGATTCTCTTCAGAGCAGCTCCCTGGCAAGACTCAAGCGCTGACACATTAATA 780

QY 781 gagaagatacaaaaaatttggtaacacaaagaatactccatctgaagctctctfag 840
 Db 781 GAGAGATATCAAAAAATTTGGTGTACACCAAAAGAAATCTCCCATTTGAAGCTCTTGAG 840

QY 841 aacttccagaggagatggaacactacactcgaatagtcaagcgactggaactctcttga 900
 Db 841 AACTTCCAGAGGAGATGGCAACTACTCTCGATATGTCAAGGCGACTGGAACCTTTGAA 900

QY 901 aaactcgaattatgagatttaaggaacctcttcaagaactcttggaaaagaagcttac 960
 Db 901 AAACCTGATATATGATTTTAACGACCCCTTTCACAGACCTCTTTGAAAAGAAAGGCTAC 960

QY 961 accttgactatgctatgattgtgtggaagactatctctactcgaatgaggtcaggtc 1020
 Db 961 ACCTTTGACTATGCTATGATGTGGGTGGAGACCTTATCTCTACTCCAGTAGGGTCAAGTT 1020

QY 1021 cactgatatctctgtgcatctgcaataactcgagaagaagccacacataaggtatcgcca 1080
 Db 1021 CACTGATATCTGTGTCATCTGCAATTAATCGAAGAAAGCCACACATAGGATCGGCCA 1080

QY 1081 tcacaacagcagctctctcgaaatcaagtggttgcctcaacaaatggaagctgaaatgtc 1140
 Db 1081 TCACAAACAGCAGCTCTTCGAAATCAAGTGTGTGCTCAACCAATGGAAGCTGAATGT 1140

QY 1141 gatgatccacaggagaccacactccatgcaacaaatcaacgtcatgcccgaagtgtagta 1200
 Db 1141 GATGATCCACAGGAGAGCCCACTCCAAATGCAACATTCACAGCTCATGCCGAGTGAAGTA 1200

QY 1201 gtggaagaagctaaigtctgtctgttctttaaagaagaagaagaagactgctcaagcgc 1260
 Db 1201 GTGAGAGAGAGTAAAGTGTGTCTGTTCTTTAAGAGGAAGAAAGAAAGAGACTGCTACGCC 1260

QY 1261 cacaagtga 1269
 Db 1261 CACAAGTGA 1269

RESULT 2
 AX250158 1269 bp DNA linear PAT 28-SEP-2001
 LOCUS AX250158 Sequence 3 from Patent WO0166594.
 DEFINITION AX250158
 ACCESSION AX250158
 VERSION AX250158.1 GI:15864533
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1269)
 AUTHORS Ploman, G.D., Whyte, D., Manning, G., Sudarsanam, S. and Martinez, R.
 TITLE Human protein kinases and protein kinase-like enzymes
 JOURNAL Patent: WO 0166594 A 3 13-SEP-2001;
 Sugen, Inc. (US)
 FEATURES
 source 1. 1269
 1. .1269
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 390 a 284 c 297 g 298 t
 ORIGIN

Query Match 100.0%; Score 1269; DB 6; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggaccatcctagtaggaagaagatgaaagacagacacaaacccaatgacaa 60
 Db 1 ATGACACATCTCTAGTAAAGAAAAGATGAAGAACACGACCAATCAACCATGGACAA 60

QY 61 aggaagtcacacgtctctgacacacatctgctccatcgtctctcttggtcttatgtg 120
 Db 61 AGGAGTCACACCTCTCTGACCAATGCTGCTCTCATGCTCTCTGGGGTCTTATGCTG 120

QY 121 ggaaccaactcaaggtctgcaagaagataagatgctggaacttcggaagctcagatta 180
 Db 121 GGACCCAACTTCAGAGGTTGGCAAGATAGATGTGGAACTTCGGAGACTCAGATTA 180

QY 181 ggtaaaaatctctacaccaaataatgtagcaatcaactggaaacaaataacacgt 240
 Db 181 GGTAAAAATCTCTACACCAATGAATATGTAGCAATCAAACTGAAACCAATTAACGT 240

QY 241 gttcccaagctctcttaagaagtagacaattatataacgtctggcagtgcgatgaagt 300
 Db 241 GCTCCACAGCTTCAATTAGAGTACAGATTTTATTAACAGCTTGGCAAGTGAAGGT 300

QY 301 ctcccaaggtgtagtaactcttgacacatgtggaataataatgcatgtgtcagatc 360
 Db 301 CTCGCCAGAGGTATTAATTGGACATGTGGAAATATATATGCGATGCTCTGGACTC 360

0Y 301 ctcccacaggtgattactcttgagccatgctgggaataataatgcatgctgctgagctc 360
|||||
Db 413 CTCGCCAGGAGTATTAATTCTTGACCATGTGGAAATATATATGCGATGCTCGAGCTC 472
0Y 361 ctgggcccctgcttgaggactctgttgacctctgtgaccggaacatttactttgaagc 420
|||||
Db 473 CTGGCCCTGCTGGAGGAGCTGTTGACCTCGTGTGACCGAAATTTACTTTGAAGAG 532
0Y 421 gcttaataatgac 480
|||||
Db 533 GTGTATATGATAGCATCCAGCTCTCTTCGAAATGGAATACGTGCACTCAAAACACTC 592
0Y 481 attaccagagatgcaagcagagaaactctccgtatgtgtgacaaaggcaataagaagag 540
|||||
Db 593 ATTACCGAGATGTCAGGACGAGAACTCTGATGTGTGACAAAGCAATTAAGAAAGAG 652
0Y 541 catgtataacatataagactcttgagctgccaagaataacatctgccccgaacccaa 600
|||||
Db 653 CATGTTATACATTAATAGACTTTGAGCTGGCCAAAGAAATACATTTGACCCGAAACCAA 712
0Y 601 aaacacatccttataaggaacacacacacacacacacacacacacacacacacacac 660
|||||
Db 713 AAACACATACCTTATAGGACACACAAAGTTTAATCTGMACTGCAATATATCTATC 772
0Y 661 aacacgcatcttgcaaaagcaaaagccggagagatgatttggaagccctagggccatag 720
|||||
Db 773 AACGCGATCTTGCAAAAGCAAAAGCCGGAGAGATGATTGGAAGCCCTAGGCCATATG 832
0Y 721 ttaatgattctccttgaggacacccctccctgcaagagactcaaggctgacacattaaa 780
|||||
Db 833 TTGATGATTTCTTCCAGGACAGCTCCCTGGCAAGAGACTCAAGGTGACATTTAAA 892
0Y 781 gaagagataaaaaaatgtgtgacacacacacacacacacacacacacacacacacac 840
|||||
Db 893 GAGAGATATCAAAAATTTGGTGACACCAAAAGAAATCTCCATGTGAAGCTCTGTGAG 952
0Y 841 aacttcacagagagatgcaaacctacactctgacatgctgagcgactggaactcttgaa 900
|||||
Db 953 AACTTCCAGAGGAGATGGCAACCTACTCGATATGTGAGGCGACTGAGACTCTTGAA 1012
0Y 901 aaactgataatgattttaaagacccctcttcacacacacacacacacacacacacac 960
|||||
Db 1013 AAACCTATTAATGATTTTAACGACCCCTCTTCACAGACCTCTTGAAGAAAGAGGTAC 1072
0Y 961 accctgacatgctgactgattggttgaggagacacttctcactcgaatgaggtcagt 1020
|||||
Db 1073 ACCTTACTATGCTTATGATGGGTGGAGACCTATCTCTACTCCAGTGGGTCACTT 1132
0Y 1021 caagtgaatctggtgcatctgcaataactcgagaagaagccacacacacacacacacac 1080
|||||
Db 1133 CAGTATATCTGCTGATCTGCATGCAATACTCGAAGAAAGCCACACATAGGGATCGGCA 1192
0Y 1081 tcacacacagacgctcttgcaaatcaggtgtgagctcaacacacacacacacacacac 1140
|||||
Db 1193 TCACAAACAGAGAGCTCTTCGAAAATCAGGTGTGCTCAACCAATGAGACCTAAAGTT 1252
0Y 1141 gatgatccacggagagac 1200
|||||
Db 1253 GATGATCCACGGAGGCCACTCCAAATGACACCAATCAAGCTCATGCCGAGGTGAGGTA 1312
0Y 1201 gctgaggaagactaagctgctgcttctttaaagagaagaagaagactgctcaagc 1260
|||||
Db 1313 GTGAGAGAGAGTAAAGCTGCTGCTGCTTTTAAGAGAAAGAGAGAGAGAGCTCAGGCG 1372
0Y 1261 cacaagctga 1269
|||||
Db 1373 CACAAGTGA 1381

RESULT 4
AX202217 AX202217 1968 bp DNA linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0153493.

ACCESSION AX202217
VERSION AX202217.1 GI:15392000
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Donoho, G., Hilpun, E., Turner, C.A., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
TITLE Human kinase protein and polynucleotides encoding the same
JOURNAL Patent: WO 0153493-A 3 26-JUL-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source
1. 1968
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 539 a 482 c 473 g 474 t
ORIGIN

Query Match 100.0%; Score 1269; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 atggaccatcctagtaggaagaagatgaaagacacagacacacacacacacacacacacac 60
|||||
Db 50 ATGACCATCTCTATAGGAAAGAAAGATGAAGAACACAGCACTAAACCATGACGACAA 109
0Y 61 aggaatgcaactgctctgac 120
|||||
Db 110 AGGAGTGCACACTGCTCTGACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 169
0Y 121 ggaac 180
|||||
Db 170 GGACCCAACTTCAAGGCTTGGCAAGAAATAGATGTGGAACTCGGAGAGCTAGATTA 229
0Y 181 gataaaatctctac 240
|||||
Db 230 GGTAAATCTCTACACCAATGAATATGATGCAATCAAACTGAAACCAATTAATCACT 289
0Y 241 gctcacaagctcatttaagtagaagattataaagaacacacacacacacacacacacac 300
|||||
Db 290 GCTCCACAGCTTCAATTAAGATGACAGATTTATTAACGCTGACAGTGCAGGTGAAGT 349
0Y 301 ctcccacaggtgatacttacttgacacatgctggaataataatgcatgctgctgagctc 360
|||||
Db 350 CTCGCCAGGAGTATTAATTCTTGACCATGTGGAAATATATATGCGATGCTCGAGCTC 409
0Y 361 ctggccctagcttgaggagactctgtgacctctgacacacacacacacacacacacacac 420
|||||
Db 410 CTGGCCCTGAGCTTGGAGAGACTGTTGACCTGTGACCGAACAATTTACTTTGAAGAG 469
0Y 421 gcttaataatgac 480
|||||
Db 470 GTGTTAAATGATAGCATCCAGCTCTCTTCGAAATGGAATACGTGCACTCAAAACCTC 529
0Y 481 attaccagagatgcaagcagagaaactctctgattgtgacacacacacacacacacacac 540
|||||
Db 530 ATTACCGAGATGTCAGGACGAGAACTCTGATGTGTGACAAAGCAATTAAGAAAGAG 589
0Y 541 catgtataacatataagactcttgagctgccaagaataacatctgccccgaacccaa 600
|||||
Db 590 CATGTTATACATTAATAGACTTTGAGCTGGCCAAAGAAATCAATTGACCCGAAACCAA 649
0Y 601 aaac 660
|||||
Db 650 AAACACATACCTTATAGGAAACACAAAGTTTAATCTGAACTGCAATATATCTATC 709
0Y 661 aacacgcatcttgcaaaagcaaaagccggagagatgatttggaagccctagggccatag 720
|||||
Db 710 AACGCGATCTTGCAAAAGCAAAAGCCGGAGAGATGATTTGGAAGCCCTTAGGCCATATG 769

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT
Db 721	ttcagtttcttcctcggaggagcctccctcgtggaaggaactaagaagctgacacattaaa	780									
Db 770	ttcagtttcttcctcggaggagcctccctcgtggaaggaactaagaagctgacacattaaa	829									
Db 781	gagagataccaataattggtgtacacccaagaatactcccatggaagctctcgtgag	840									
Db 830	gagagatattcAAAAAATTGGTGACACCAAAAGAAATACCTCCATTGAACTCTGTAG	889									
Db 841	aacttccagagagatgagcaactacacttcgatalgttcagggcgactgactcttga	900									
Db 890	AACTTCCAGAGAGAGATGGCAACCTACCTGATATGTCAGGCGACTGGACTTTTGA	949									
Db 901	aaactgattatgattatcagagacactcttcacagacactcttggaaaagaagctac	960									
Db 950	AAACTGTATTATGATATTATTCGGACCCCTCTTCACAGACCTCTTTGAAAAGAAAGCTAC	1009									
Db 961	accttgactctgcctatgattgggttgggaacctatttcctacacagtaaggtcagtt	1020									
Db 1010	ACCTTGTACTATGCTTATGATTTGGTTTGGAGACCTATTCTCACTCCAGTACGATG	1069									
Db 1021	cacgtagaattctggtgacatctgcaataactcgagaagaacacacacataaggtatcgca	1080									
Db 1070	CACGTAGATTTGCGTGACATCTGCATAAATCTGAGAAAGCACACATAGGATGGGCA	1129									
Db 1081	tcacacagcagcctcttcgaaatacgaatggtgtatgctcaaccaatgagagctgaattt	1140									
Db 1130	TCACACAGCAGCAGCCCTCTGCAAAATAGGTGTGTACTCAACCAATGGAGAGCTGAATGT	1189									
Db 1141	gatgtccacagggagggccacatccaatgcacacacacagctcatgcccgaagtggagta	1200									
Db 1190	GATGATCCACAGGGAGGCCCACTCCAAATGCACCAATCAGCTCATGCGGAGGTGGAGTA	1249									
Db 1201	gtgagagagagcctaagtctgctgttctttaaagagaaagaaagaaagctcagcgc	1260									
Db 1250	GTGGAGGAAGCTAAGTGTGCTGTTCTTTAAAGAGAAAGAAAGAAAGAGAGCTCAGGCG	1309									
Db 1261	cacaagtga 1269										
Db 1310	CACAAGTGA 1318										
RESULT 5											
LOCUS	BC017236	2066 bp	mRNA	linear	PRI 09-NOV-2001						
DEFINITION	Homo sapiens, casein kinase 1, gamma 1, clone MGC:19461										
IMAGE	4123494, mRNA, complete cds.										
ACCESSION	BC017236										
VERSION	BC017236.1	GI:16878051									
KEYWORDS	MGC.										
SOURCE	human.										
ORGANISM	Homo sapiens										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.										
TITLE	1 (bases 1 to 2066)										
JOURNAL	Strausberg, R.										
	Direct Submission										
	Submitted (05-NOV-2001) National Institutes of Health, Mammalian										
	Gene Collection (MGC), Cancer Genomics Office, National Cancer										
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,										
	USA										
	NIH-MGC Project URL: http://mgc.ncl.nih.gov										
	Contact: MGC help desk										
	Email: cgabds-remail.nih.gov										
	Tissue Procurement: ATCC										
	cDNA Library Preparation: Rudin Laboratory										

Query Match	Best Local Similarity	Matches 1198:	Conservative	Score 1198:	DB 9:	Length 2065:
				Pred. No. 0:	Mismatches	Indels
					Gaps	0:
72	ctgcctcgaccatctggtctccatctgctccctctggtgtctctatggtggaccactt	131				
10	ctgctctgaccatctggtctccatctgctccctctggtgtctctatggtggaccactt	69				
132	cagggttgcaagaagatagagatggtggaactctggaagctccaattaggttaaaatct	191				
70	cagggttgcaagaagatagagatggtggaactctggaagctccaattaggttaaaatct	129				
192	ctacaccaatgaaatctagcaatcaaacctggaaccaataaaatcagtgctccacagct	251				
130	ctacaccaatgaaatctagcaatcaaacctggaaccaataaaatcagtgctccacagct	189				
252	tcatttaagtaacagattttaaacacgtctggagctcaggtgaaggtctccaccaggt	311				
190	tcatttaagtaacagattttaaacacgtctggagctcaggtgaaggtctccaccaggt	249				
312	gtattactctggacacatggtggaataataaatgccaatggtctggaagctcccttgccctag	371				
250	gtattactctggacacatggtggaataataaatgccaatggtctggaagctcccttgccctag	309				
372	ctggaagacttggttgacctctgacccgaacattacttgaagacggtgttaagat	431				
310	ctggaagacttggttgacctctgacccgaacattacttgaagacggtgtgttaagat	369				
432	agccatccagctctctctgaaatggaatagtggaacccaaagaacctcattaccgga	491				
370	agccatccagctctctctgaaatggaatagtggaacccaaagaacctcattaccgga	429				
492	tgtcaagacagaaactctcgtatggtgcgaagaagcataagaagaagcattatataca	551				
430	tgtcaagacagaaactctcgtatggtgcgaagaagcataagaagaagcattatataca	489				
552	cattataactttgactgcgcaagaatacatatgaccgccgaatacaaaaacacatacc	611				

|||||
Db 490 CATATAGACTTGGAGCGCAAGAAATACATGACCCCAACCAACAAACATACAC 549
QY 612 ttatagggaacacaaagttaacttgatgacgcgaagataatgtctatcaacacgcatct 671
Db 550 TTATAGGGAACACAAATTTAACTGGAAGTGAAGATATATGCTATCAACACGCAATCT 609
QY 672 tggcaaaagacgaacgcgagagatgatttggaaagcccttaagccatattgtcatgattt 731
Db 610 TGGCAAGAGCAAGCCGAGAGATGATTTGAAAGCCCTAGGCCATATGTTGATATTT 669
QY 732 ccttcgagcagcctccctcggcaagacatcaaggctgcaacattaaagagatataca 791
Db 670 CCTTCGAGGAGCCTCCCTCCGCAAGACTCAAGCTGACACATTTAAAGAGATATCA 729
QY 792 aaaattggtgacacacaaagaaatactcccatgaaagctctcgttgaacattccaga 851
Db 730 AAAATTTGGTACACCAAAAGAAATCTCCCATTTGAAAGCTCTCTGTGAACTTTCCAGA 789
QY 852 ggaagtgcgaac 911
Db 790 GGAATGGAACCTACCTACCTGATATGTCAGCGACTGACTTTTGAAGAAACCTGATTA 849
QY 912 tgaatattacgagacccctctcagacacacacacacacacacacacacacacacacac 971
Db 850 TGAATATTTACGAGACCCCTCTTACAGACACCTTTGAAAGAAAGAGCTACACCTTTGACTA 909
QY 972 tgcctatgattgggttggagaaacacacacacacacacacacacacacacacacacac 1031
Db 910 TGCCTATGATTTGGTGGAGACCTATTTCTACTCCATGAGGTGATGCTACAGTATTC 969
QY 1032 tggatcatctgacaaatactcagaaagacacacacacacacacacacacacacacacac 1091
Db 970 TGGTGCATCTGCATTAATCTGAGAAAGCCACACACATAGGAGTGGCCATCAACAGACA 1029
QY 1092 gctcttcgaaatacagtggttgaagctcaacaaatgagagagctgaatgttgaatccac 1151
Db 1030 GCCCTTTCGAAATAGAGGTGTTAGCTCAACCAATGAGAGTGAATGTGATGATCCAC 1089
QY 1152 gggagccac 1211
Db 1090 GGGAGCCCACTCCAAATGACCAATACACAGCTCATGCGGAGGTGAGGTGAGGAGAGC 1149
QY 1212 taagtgcgtctgtcttctaagagaaagaaagaaagaaagaaagaaagaaagaaagaa 1269
Db 1150 TAACTGCTGCTGTTCTTTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1207

RESULT 6
AX239864 4417 bp DNA linear PAT 26-SEP-2001
LOCUS AX239864
DEFINITION Sequence 4 from Patent WO0164905.
ACCESSION AX239864
VERSION AX239864.1 GI:15797470
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 4417)
AUTHORS Olandt,P.J., Kapeller-Libermann,R. and Meyers,R.A.
TITLE 2504, 15977, and 14760, novel protein kinase family members and
uses thereof
Patent: WO 0164905-A 4 07-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Source
1..4417
/organism="Homo sapiens"
/db_xref="taxon:9606"
337..1716
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC88317.1"

/db_xref="GI:15797471"
/translation="MDPSREKDERQRTTRPMQSRHCSRPSGSSSSGVLWGPNF
RVGKKIGCNFGLRLKLNLYNEVYAIKLEPIKSRAPQLHLEYREFKQSGSEGLP
OVYFEGCGKNAMVLEPSELEDLDLDREFTEKTVLMILSLSPREYHKNL
IYRVKPENFLIGROGKKEHVHIIIDFGAKETIDETKHIIPYRHSILTGARML
SINHLEKESRRDDLEALHMEPYRFGLSLPNOGLKADPLKRYOKLIGTKNTPE
ALCENFEEMATYLRVRLDFFERKPYEPLRTPLPEKKGTPEYADWDGRPLP
TPGVSFVHDSGASATRESHTHDPSPQOQPLRNQNVSSERGEWEIOPSQNTSTL
TSHLAQRHSGSVQVVSSTNGELNVDPPTGASHSNAPITAAAEVEAEKCCFEKKR
RKTAQRHK"

BASE COUNT 1241 a 1006 c 1065 g 1105 t
ORIGIN
Query Match 90.3%; Score 1146.4; DB 6; Length 4417;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1268; Conservative 0; Mismatches 1; Indels 111; Gaps 1;
QY 1 atgagccatcctagttaggaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 60
Db 337 ATGACCATCTCTAGTAGGAAAGAGTGAAGACAAACGACACCTAAACCCATGGCACAA 396
QY 61 aggaatgacacacgtctcgcgac 120
Db 397 AGGAGTGCACACTGCTCTCGACCATCTGCTCTCATCTGCTCTGAGGCTCTTATGCTG 456
QY 121 ggaaccaactcagaggttgcgaagaagataagatgtggaacttcggaagctcagatla 180
Db 457 GGACCCAACTTCAGGGTGGCAAGAAAGATAGAGTGGAACTTCGAGACTCAGATTA 516
QY 181 ggtaaaactctcac 240
Db 517 GGTAAAATCTCTACACCAATGAATATGTACCAATCAACCAACCAATTAATACACT 576
QY 241 gctccacagctcatttagagatacagatttaataacacagcttcggaagctcagagtgaaagt 300
Db 577 GCTCCACAGCTTCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 636
QY 301 ctccacacagtgatattacttgcgaacacacacacacacacacacacacacacacacacacac 360
Db 637 CTCACAGAGGTATTTAGTACAGATGAGGAAATATATGATGATGATGATGATGATGATG 696
QY 361 ctggccctacgttggaagacttggtaacctcgtgcggaacacacacacacacacacacacac 420
Db 697 CTGGCCCTTACCTGGAGAGACTTGTGTGACCTGCTGTCGCAACATTTACTTTGAAGCG 756
QY 421 gtttaaatgataagcaccac 480
Db 757 GTGTTAATGATAGCCATCACTGCTCTTCTGAAATGGAATGATGATGATGATGATGATG 816
QY 481 attacagagatgtcaagcagagaacttcctgatttgcgacaaggaataagaagaag 540
Db 817 ATTATCCAGATGATCAACCCAGAGAACTTCTGATGATGATGATGATGATGATGATGATG 876
QY 541 catgtataacacattatagacttggagctggcgaaggaataattgaccgccgaacacaa 600
Db 877 CATGTTATGACATTTATGACTTTGGACTGTCGCAAGGAATCATTTGACCCGAAACCAA 936
QY 601 aaacacacacattataggaac 660
Db 937 AAACCATACCTTTATAGGAACACAAAGTTTAACTGCAACTGCGAAGATATATGCTATC 996
QY 661 aacacgcactcttgcgaagaagcgaagcgaagagatgatttggaaagccctagacatg 720
Db 997 AAACGCGATCTTGGCAAGACCAAGCCGAGAGATGATTTGAAAGCCCTAGGCCATATG 1056
QY 721 ttcaatgttctccttcgaggaagcctccctcggcaaggaacacacacacacacacacacacac 780
Db 1057 TTCAATGATTTCTTCGAGGAGCCTCCCTGCGCAAGGACTCAAGGCTGACACATTAATA 1116
QY 781 gagagatacaaaaatgtgtac 840
Db 1117 GAGAGATATCAAAAATTTGTGACACCAAAAGGAATATCTCCATGTGAAGCTCTGCTGAG 1176

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
QY 841	AX339866	Sequence 6 from Patent WO0164905.	AX339866	1	GI:15797472	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Olandt, P.J., Kapeller-Jbermann, R. and Meyers, R.A.	2504, 15977, and 14760, novel protein kinase family members and uses therefor.	Patent: WO 0164905-A 6 07-SEP-2001; Millennium Pharmaceuticals, Inc. (US)	1. 1377 Location/Qualifiers	418 a 315 c 328 g 316 t	
QY 901	1177	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1177	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 901	1237	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1237	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 901	1297	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1297	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1021	1357	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1357	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1081	1417	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1417	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1105	1477	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1477	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1105	1537	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1537	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1150	1597	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1597	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1210	1657	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1657	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1269	1716	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1716	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1269	1716	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1716	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1269	1716	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1716	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	900	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga	1236	aaacttcagagaaatgagcaaaccttcgatgtatgcagagcagctgactctttga
QY 1269	1716	aaacttcagagaaatgagcaaacct												

Db	61	AGAGTGCACACTCTCTCCAGACCATCTGGCTCTCATTGCTTCGCTTGGGTTCTTATGGTG	120
Qy	121	ggaccacattcaaggttggcaagaagaatagaatgtgggaacttcggagactcagatla	180
Db	121	GGACCACACTTCAAGSGTTGGCAAGAAATATGTGATGTGGGAATCTCGGAAGCTCGATTA	180
Qy	181	ggtaaaaatctctcaccacaatgaatatgtgcaatcaaaacttgaacaaataaacagct	240
Db	181	GGTAAAAATCTCTACACCACCAATGAATATGTGTGCAATAACTGGAAACCAATAAATACGCT	240
Qy	241	gtccacagcttcaattagagtaacagaattataaacagcttgcagtcagttgaagt	300
Db	241	GCTCCACACGCTTCAATTATAGATACAGATTTATTAACACGCTTGGCAGTGCAGGTGAAGT	300
Qy	301	ctcccccacagtgatlaactatttggaccaatgtgggaaatataatgcatalgtgtcgtgac	360
Db	301	CTCCACAGAGTGATATTAATCTTTGGACCATGTGGGAAATATATATGCAATGCTGTGGAGCTC	360
Qy	361	cttggccctagcttggaggaacttgttttgaacctctgtgacccgaacctattactttgaagc	420
Db	361	CTTGGCCCTTACTCTTGGAGGACTTGTTTGACCTCTGTGACCGAACATTTACTTTGAAGACG	420
Qy	421	gtgttaataagatagacatccacagctgcctcttcgaaatgaatacgtgcacccaagaacctc	480
Db	421	GTGTTAATAGATAGCCATTCACAGTCTCTTCTTCGATATGGAATAGTACGTGCATCAAGAACCTC	480
Qy	481	attacccgagatgtcacaagccagaagaacttctcgtattgtgtgcacaagcacaataagaag	540
Db	481	ATTTACCGAGATGTCAAGCCAGAGAACTTCTGATTGTGTGCACAAAGCAATTAAGAAAGAG	540
Qy	541	catgtataacatataagacttttgaactgtgccaaggaatacatgtgaaccccgaaaccaa	600
Db	541	CATGTATATACACTAATTAAGACTTTGTGACTGTCCCAAGGAATACATTGACCCCAAAACAAA	600
Qy	601	aaacacacactttagggaaacaaaagtattacctgggaactcgaacataatattgtctatc	660
Db	601	AAACACATACCTTTATAGGGAACACAAAAGTTTAACTGGAATCTCGAGATATATGTCTATC	660
Qy	661	aacacgcactcttgcacaaagcaagaacgcggagagatgtatttgaagcccttaggcatalg	720
Db	661	AAACGCACTCTTGCCAAAGCAAGCCGGAGAGATGATTGGAAACCTTAGGCCATATAG	720
Qy	721	ttcatgtattccttccttgaagcagcctccctctgccaaggaactcaaggcttgaacatlaaa	780
Db	721	TTTCATGTATTTCTTCCGACAGCAGCTCTCCCTGGCAAGACTCAAGCTGTACACATTAA	780
Qy	781	gagagataatcaaaaatttgttgaacccaagaagaataaccccatitgaactctctgttag	840
Db	781	GAGGATATCAAAAATTTGGTGACACCAAAAAGAAATACCTCCATTGAACTCTCTGTGAG	840
Qy	841	aacttccagaagagatgtgcgaacctaactctcgaatagtcaagcgaactgtacttcttga	900
Db	841	AACTTCCAGAGGAGATGGGCACTCACTCGATATGTCAAGGGACTGACATTCTTGAA	900
Qy	901	aaacttgattatagratltaaggaacctcttcaagacctcttgaagaagaagctaac	960
Db	901	AAACCTGATTTATGTGATTTTACGAGACCTCTTACAGACCTCTTTGAAAAGAAAGCTAC	960
Qy	961	aactttagacttgcacttgaatttggatggagaacctaactccactaacccaatgaagtcagtt	1020
Db	961	ACCTTTGACTATGCTATATGATTTGGGTTGGAGACCTATTTCTTACTTCACTAGGTAGGATCAGTT	1020
Qy	1021	cacgtagatltctgtgatcatgcataaactcggaaagccacacacataaggaatgcgca	1080
Db	1021	CACGTAGATTCTGTGATGTGCAATATACTCGAGAAAGCACACATATGGGATCGGCCA	1080
Qy	1081	tcacaacagcagcctcttcgaaat-----	1104
Db	1081	TCACAACAGCAGCCTCTTCCAAATCAGAAATGTATCATCAGAGCGCGAGAGATGGGAA	1140
Qy	1105	-----	1104
Db	1141	ATTACGCCACCGCGACACCAATTAACCTCACTAAGCTCTCACTTGGCTGCAGACCGC	1200


```
QY 1105 -----caggtggttaagtcacccaatgagagagctgaatggttcatgcatcc 1149
1201 CATGGGGATCATGTCAGAGGTGTTAGCTCAACCAATGAGAGCTGAATGTTGATGATCC 1260
QY 1150 acggagagccatccatgacccaatgacagctcatgctgaggtgaggtgagagaa 1209
1261 ACGGAGCCCATCTCAATGACCAATGACAGCTCATCCCGAGGTGAGAGTGTGAGAGAA 1320
QY 1210 gctaaagctgctggttctttaaagagaaagagagctgctgacccacaaag 1266
1321 GCTAAGTGTGCTGTTCTTTAAGAGGAAAGAGAGAGCTGCTCAGCCGACAG 1377
RESULT 8
AB042562 1950 bp mRNA linear PRI 23-JAN-2001
LOCUS AB042562 Homo sapiens CSNK1G1 mRNA for casein kinase 1 gamma 1, complete
DEFINITION cds.
ACCESSION AB042562 GI:11177007
VERSION AB042562.1
KEYWORDS Homo sapiens cDNA to mRNA, clone_l1b:lambda ZAP human testis
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites) Hirai, M., Tanuma, R. and Hashimoto, K.
AUTHORS Kusuda, Y.
TITLE Cloning, expression analysis and chromosome mapping of human casein
kinase 1 gamma (CSNK1G1): identification of two types of cDNA
encoding the kinase protein associated with heterologous
carboxy-terminal sequences
JOURNAL Cytogenet. Cell Genet. 90 (3-4), 298-302 (2000)
PUBMED 11124537
REFERENCE 2 (bases 1 to 1950)
AUTHORS Kusuda, Y.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Jun Kusuda, National Institute of
Infectious Diseases, Division of Genetic Resources; 1-23-1,
Toyama-cho, Shinjuku, Tokyo 162-8640, Japan
(E-mail: jkusuda@nih.go.jp, URL: http://www.nih.go.jp,
Tel: 81-3-5285-1111 (ex. 2122), Fax: 81-3-5285-1181)
location/Qualifiers
source 1. 1950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Lambda ZAP human testis cDNA(Stratagene,
No.939201)"
/note="vector:pHCK1G1-5"
129. 1310
/gene="CSNK1G1"
129. 1310
/gene="CSNK1G1"
CDS
129. 1310
/gene="CSNK1G1"
/product="casein kinase 1 gamma 1"
/codon_start=1
/db_xref="GI:11177008"
/translation="MDHPRSEKDERORTTKPMQRSNHCSPGSSSSGVIMVGPVF
RVGKRTGCGNFGELRLGKNLYTNEYVAIKLEPTKSRAPOLHELYRYKQIGSAGEGIP
QVYTFPGCGKYNNAMVLELLGPLELDELCDRTFTKTYMIAIQLSRMEYHSKUL
IYRDVAPENFLIGROGKNEHVHIIDFGLAKKEYIDPETKHHIPREHKSILGTARYM
SINTHLGKESRRDDELALGKHMVFLRGLPMQGLKADTLKRYOKIGDKRNTPIE
ALCENPREMATYLRVRLDFEKKPDYELFTFDLEFKKGYTDDYADWVGPRIP
TPVGSYHVDGSAITRSHTRHSDRPSQOPLANOSLRVTATAHYVNNNAIWHRGCG
T"
```

BASE COUNT 569 a 454 c 467 g 460 t

ORIGIN

Query Match 87.7%; Score 1113; DB 9; Length 1950;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```
QY 1 atggaccatccctagtagggaagaagatgaaagacacgacgaacaaatccatgacaa 60
129 ATGACCATCTCTAGTAGGGAAGAAAGATGAAGAACAGACCAACTAAACCATAGGCACAA 188
QY 61 aggaagtcacacacgctcttgacccaatcgtctccatccatccctcgtggtcttaagtg 120
189 AGGAGTGCACACATGCTCTTCACCATCTGCTCCCATCGTCCTGCGGTTCTTATAGGTG 248
QY 121 ggaaccacactcaaggtctggaagaagataagatggtggaactcgaagagctcaga 180
249 GGACCCACTTCACAGGTTGGCAGAAAGATAGATGTGGAACTTCGAGAGCTCAGATTGA 308
QY 181 ggtaaaaatctctacacaaatgaaatgtagcaatcaactggaaccaataaaatcaagt 240
309 GGTAAATCTCTACACCAATGAAATATGTAGCAATCAAACTGGAAACCAATAAATCAGT 368
QY 241 gctccacagcttcatttaagagtaagaatttataaacagcttggcagtgagtgaaagt 300
369 GCTCCACAGCTTCATTTAGAGTACAGATTTTATTAAGAGCTTGCGACGTGAGGTAAGGT 428
QY 301 ctcccaaggtgtaattactcttgagccaatgtaggaataatagccatggtcgtgagctc 360
429 CTCACAGAGTGTATTAATCTTTGACACATGTGGAAATATATGCTATGTGCTGAGCTC 488
QY 361 ctggccctagcttggaagacttggtaacctctgtgacccaacttaacttgaagagc 420
489 CTGGCCCTAGCTTGAGAGACTTGTGTGACCTGTGACGAACTATTACTTTGAAGAGC 548
QY 421 ggttaatgataacatccacagctgctctccgaatgaaatgacgtgacctaagaagactc 480
549 GTGTTAATGTATAGCATTCAGCATCGCTCTTCTCGAATGGAATACGCTCTAAAGAACCTC 608
QY 481 attacacagatgacagacgaagaactcctgattggtgcagacgaagcaataagaagag 540
609 ATTACCGAGATGTCAAGCCAGAGAACTTCTGATTGTGTGACAGCAATTAAGAAAGAG 668
QY 541 catgtaacacatataagacttggacctggcccaaggaatacatltagcccgaaaccaa 600
669 CATGTATACATTAATATAGACTTTGAGCTGACCAAGAAATATGATGACCCGAAACCAA 728
QY 601 aaacacacaccttaaggaagacacaaaagttaactctggaactgaaataatagtctatc 660
729 AAACACATACCTTATAGGGAACACAAAGTTTAATCTGAATCGCAATATATGCTATC 788
QY 661 aacacgacatcttgcaagaagcaagccgagagagatgatttgaagccctcaggccatatg 720
789 AACACGATCTTGCCANAGACCAAGCCGAGAGATGATTGGAAAGCCCTAAGCCATATG 848
QY 721 ttcatgattctctcgagcagcctccctcgtgcaaggaactcaaggtgacacattaaa 780
849 TTCAATGATTTCCTTCGAGGAGAGCTCCCTGGCAAGAGACTCAAGGCTGACACTTAA 908
QY 781 gagaagatacaaaaattggtgacacaaagaatactcccatgtaagctctctgtgag 840
909 GAGAGATATCAAAAATTGTGACACCAAAAGGATATCTCCCATGTAAGCTCTCTGTGAG 968
QY 841 aacttcagaagagatgagcaacctacccttcagatatgcaaggcgacggaactcttgaa 900
969 AACTTTCCAGAGGAGATGGCACTACCTTGATATGATCAAGGCACTGAGACTTCTTGAA 1028
QY 901 aaactgattatgagatlttaaggacccctctcacaagacctcttgaagaagaagcttac 960
1029 AAACCTGATTATGAGTATTTACGAGACCTCTTCAACAACCTTTGAAAAGAAAGGCTAC 1088
QY 961 accttgacctatgacctatgattggttggaagaccttctctactcaagtaggtgagtt 1020
1089 ACCTTTACTATATGCTATGATGAGTGGTGGAGACCTATTCCTATCCAGTAGAGGTACATT 1148
QY 1021 caactagatctggtgacatctgcaataactcagagaagaagccacacataagagatcgcca 1080
1149 CACGTAGATTCTGTGTCATCTGCAATGAACTCGAATAAGCCACACATATAGGAGATCGGCA 1208
```

QY 1081 tcacaacagcagcctctgcgaatcaggtgtagctcaaccaatgagagcgtgatt 1140
|||||
Db 1209 TCACAAAGCAGCGCTCTCGAATAATGACGCTTAGAGCTGTACAGCTGAGCATTTATGAT 1268
QY 1141 gatgatccacg 1153
|||
Db 1269 GTTAAACAATCAG 1281

RESULT 9
RNU22296 1648 bp mRNA linear ROD 09-JUN-1995
LOCUS Rattus norvegicus casein kinase 1 gamma 1 isoform mRNA, complete
DEFINITION cds.
ACCESSION U22296
VERSION U22296.1 GI:854732
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (Bases 1 to 1648)
AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
TITLE Casein kinase 1 gamma subfamily. Molecular cloning, expression, and
characterization of three mammalian isoforms and complementation of
defects in the Saccharomyces cerevisiae YCK genes
J. Biol. Chem. 270 (21), 12717-12724 (1995)
95279411

JOURNAL 2 (Bases 1 to 1648)
MEDLINE Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
AUTHORS Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
TITLE Direct Submision
JOURNAL Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular
Biology, University of Indiana School of Medicine, 635 Barnhill
Drive, Indianapolis, IN 46202-5122, USA
Location/Qualifiers

FEATURES
source 1..1648
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
CDS 288..1460
/note="protein kinase"
/codon_start=1
/product="casein kinase 1 gamma 1 isoform"
/protein_id="AAC52200.1"
/db_xref="GI:854733"
/translation="MDHSNREKDDRORTTKTMAQRTNTHCSRPSGTSSGVLVAVGPNF
RVGKRTGCGNFGELRTGKNLYTNEVAITLEPTKSRAPOLHLEYRKYDLSGSELP
OYTRPGCKRYNAMYLELGPSEDFDLCDRFTTKYTLMLTAIQLLSREYVHSKNTL
IRADVPENFLIGRGNKKEHVLIHIDFGLAKYIDPEYTKHLPYEHKSLSGTAKIM
SINTHLGKQSRDDEALGHHMFYLRSLPMQGLAKADLPKRYOKIDTKRSTPIE
ALCENPEEMETLYRVRLEDFEKKYDLYLEFLEKRYGTYDYAVDWGGRIP
TPGSVHYVDSGASAIRFRESHDRPSQQOPLNQRSLTAEWFLAPLSHPAPR"
1648
polyA_site /note="40 A nucleotides"
BASE COUNT 503 a 359 c 384 g 402 t
ORIGIN

Query Match 77.1%; Score 979; DB 10; Length 1648;
Best Local Similarity 92.8%; Pred. No. 3.1e-280;
Matches 1027; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1 atgagcaccatagtaggaagaagatgaagaacgagcaacgaacccaatgagcaaa 60
|||||
Db 288 ATGACCATCTTATATAGAAAGATGATGACACAGGACCACTAATAACATGAGCAAA 347

QY 61 agagagtgcaacgtgctcgcacacatgctcctcattcgtctctgggttcttaagtg 120
|||||
Db 348 AGGAATACACAGTGTCCGACATCTGACATTCACATCTCTGGGGTTTCATGATG 407

QY 121 ggaaccacatcaggtgtgcaagaagatagatgtgtggaacttcgagagctcagatta 180

|||||
Db 408 GGACCCAACTTCAGGGGTGGCAAGAAATAGAGGTGGGAAGCTCGGAGAGCTCAGATTA 467
QY 181 ggtaaaaatctctaacaccaatgaataatgtaacaaacttgaaacaaataaactcgt 240
|||||
Db 468 GGTAAAAATCTTACACCAATGATATGTAGCCATTAACTGGAACCAATAAAAATCTACGT 527
QY 241 ggtccagaagcttaattagaagtaacagtttataaacagcttgacgtgcaagtgaaagtc 300
|||||
Db 528 GCTCCACAACCTTCAATTAGAGTACAGGTGTTATTAACAGCTCGGACATGCAAGTGAAGGT 587
QY 301 ctccccaaggtgtaatactcttgagccatgtggaagaataataatgcaatggtctggaagtc 360
|||||
Db 588 CTCGCCAAGGTTTATATCTTGTGACCATGTGGGAAGTAAATGCAATGCTGGAATCTC 647
QY 361 ctggcccttagcttgagagcctgttctgacccctctgtacggaacattacttgaagagc 420
|||||
Db 648 CTCGGCCCTTAGCTTGAAGACTTGTGTGACCTGTGACCGAATGTTACTTTGAACAGC 707
QY 421 ggttaattgtagccatccagctgctcttcgaaatgtaacgtgcaactcaaaacctc 480
|||||
Db 708 GTGTTAATGATAGCCATCCAGTGTCTTCTGAAATGAGATGTACACTCAAGAAATCTC 767
QY 481 attaccagatgtcaagccagagaactcctcgtatgtgcagacaagcaataaagaagag 540
|||||
Db 768 ATTTACCGAATGTCAACACGACGAACTTCTTATTTGGCCGACAGCAATTAAGAAAGAG 827
QY 541 catgtatcacatlatagactcttgagctgccaaggaataacattgaccccgaaaccaa 600
|||||
Db 828 CAGTATATACAACTTATAGATTTTGGACTGGCCAAAGAAATCATTTGATCCGAAACCAA 887
QY 601 aaacacatccttatagtgagacacaaaagtttaacttgaaacttgaaatatatctc 660
|||||
Db 888 AAACACATACCTTCAACAGAGGACAAAGGCTTAATCTGAATGCGCATACATCTATC 947
QY 661 aacaagcatttgcaagaagcaagccgagagatgatttggaagccctcagagcatatg 720
|||||
Db 948 AACACATATGAGCAAAAGCAAGCAAGCGGCGGATGATTGGAAAGCCGCGCATATG 1007
QY 721 ttaatgatttcttcgagcagccctcccttgcaaggaactcaagctgacacataaa 780
|||||
Db 1008 TTGATGACTTCCCTCGAGGACGCTACCTCGCAAGGACCTGATATACATTTAAA 1067
QY 781 gaagatatataaaaattgtgtgacacaaaaggaatactccattgaagctctgtgag 840
|||||
Db 1068 GAGAGATATAGAAAATGTGTGATACCAAAAGAGTACTCCATCGAAGCTCTGTGAG 1127
QY 841 aacttccagagagatgagcaacccttcgatatgtcagggcgaactgactcttggaa 900
|||||
Db 1128 AACTTCCAGAGGAGATGAGACTTACTTGGATATGTCAGAGATATAGACTTCTTGAA 1187
QY 901 aaactgatatagatttlaacgagccctctcagagacctcttgaagaagaagctac 960
|||||
Db 1188 AAACCTGATATAGATTTTACGGAACCTCTTCAAGATGCTGTTGAACGAAGGCTAT 1247
QY 961 aacttgacatgctatagttggtgtgagagacattctcactcaagtagagtcgt 1020
|||||
Db 1248 ACTTTGACTATAGCTATGATGTGGTGGAAAGGCTTATCTTCACTCAAGTAGATCAATT 1307
QY 1021 caagttagattctgtgcatctgacataactcgaagaagcaacacataaggaatcgagca 1080
|||||
Db 1308 CATGTGATTTCTGTGATGTGCAATATACATCGAAGAAAGCCACACACAGGATCGACCA 1367
QY 1081 tcacaacagcagcctcttcgaatcag 1107
|||||
Db 1368 TCACAACACAGCCTTATGAAATCAG 1394

RESULT 10
AK026957 3552 bp mRNA linear PRI 29-SEP-2000
LOCUS AK026957
DEFINITION Homo sapiens cDNA: FLJ23304 fls, clone HEP11377.
ACCESSION AK026957

VERSION AK026957.1 GI:10439939
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:hepg2 cDNA to mRNA, clone_11b:HEP
clone:HEP11377.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (sites)
AUTHORS Kawabata,A., Hiki,I., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishl,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 3552)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishl,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdna@hims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan, cDNA full insert
sequencing: Research Association for Biotechnology: cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
source
1..3552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP11377"
/cell_line="hepg2"
/cell_type="hepatoma"
/clone_11b="HEP"
/note="cloning vector pME18SFL3"
14..856
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB15601.1"
/db_xref="GI:10439940"
/translation="MIAIQLSLMEYVHSNLIYRDVKNPFLIGRRGNKKHHVHII
DGLAKEVIDPEPKHPIYREHKSILGTATYMSINHLGEOSRDLDELALHMFME
LRSGLPMOGLKADPLKREYOKIGDTKRNPIELNPEPEATLYRYRLDFEKP
DYRYLTLFTDLDEPKKGYTFDYADWGRIRIPPVSYNHDSSASATIRSHTHDRP
SQOQPLRNQVSVSTNGELNVDPTGAHSNAPITAHAEVEVEAKCCCFKKRKKTA
ORHK"
CDS
BASE COUNT 989 a 805 c 863 g 895 t
ORIGIN

Query Match 67.2%; Score 852.8; DB 9; Length 3552;
Best Local Similarity 99.8%; Pred. No. 1.4e-242;
Matches 854; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 414 gaagacgggtttaatgataccatccagctgccttcgaatgaatacgtgacactaaa 473
DB 1 GGAACGCGTGTAAATGATAGCATCCAGCTGCTTCGAAATGGAATACGCTCAAA 60
QY 474 gaaccatattaccagaatgtcaagcagaagaactcctgattgctgcagacaagaataa 533
DB 61 GAACCTCATTTACCGAGATGCAAGCCAGAACTCTCTGATGTGCGACGAGGCATATA 120
QY 534 gaagagacatgtttaacatataagacttgagctggccagaagaataacatgacccga 593
DB 121 GAAAGACATCTTATACACATATAGACTTTGGACTGCGCAAGAAATACATTGACCCCGA 180
QY 594 aaccacaaaacacatacccttaaggaacacaaaagtttaactggaactgcaaatatata 653
DB 181 AACCAAAAACACATACCTTATAGGGAACACAAAAGTTTAACTGGAACCTGCAATATAT 240

QY 654 gtctatacaacgcatcttggcagaagcgaagccggagagatgatttggaaacctag 713
DB 241 GTCTATTCACACCGCATCTTGGCAAAAGCAGAAAGCCGAGATGATTTGGAAACCCCTAGG 300
QY 714 ccatagttcattatcttccttcaggacgctcccttcgcaaggaactcaagctgacac 773
DB 301 CCATATGTTATGATATTTCTTCAGGACACCTCCCTGGCAAGACTCAAGCTGACAC 360
QY 774 attaaagagatatcaaaaatattgtgcacacaaaggaataactccttgaaacct 833
DB 361 ATTTAAAGAGATATCAAAAATTTGGTGAACCAAAAAGAAATACCTCCATTGAAGCTCT 420
QY 834 ctgtgaaacttcacagaagagatgcaactccttcgatatgcaagcagctgacct 893
DB 421 CTGTGAAGACTTTCAGAGAGAGATGCAACCTACCTTCGATATGTCAGGAGCTGAGCTT 480
QY 894 cttgaaaaaacctgattatgattatgaagaccttcacagacctctttaaagaa 953
DB 481 CTTTGAAAAACCTGATTTATGATTTATGATTTAGACACCCCTTCACAGACTCTTTGAAAA 540
QY 954 aggtcacaccttgactatgacctatgattgtgtggaagacctatcctactcagtag 1013
DB 541 AGGCTACACCTTGTACTATGCTATGATGATGGTTGGAGACCTATCTCACTCACTAGG 600
QY 1014 gtcaagtcagtagatctgtgtcatctcaataactcgagaagacacacacatagga 1073
DB 601 GTCAAGTTCACGATGATTTCTGTGCATCTGCATTAACTCGAGAAAGCCACACATAGGA 660
QY 1074 tcggccatcaacagacgacctcttgaaatcagggtgtgtaagtcacacaaatggagact 1133
DB 661 TCGGCCATCACACAGACGCTCTTCGAAATCAGGTGTTAGCTCAACCAATGGAGAGCT 720
QY 1134 gaatgttatgatcccaaggagcccaactcacaatgcaacacacacagctcagaggt 1193
DB 721 GAATGTTGATGATGCCAGCGGAGGCCACTCCAAATGACACATCAACACTATGCCGAGGT 780
QY 1194 ggaagtgatgaggaagcctaagtcgtctttctttaaagaggaaggaagagactgc 1253
DB 781 GGAAGTAGTGAGAGAACTAAGTGTCTGTTCTTTTAAAGGAAAAAGAAAGACTGC 840
QY 1254 tcagggccacacaagtga 1269
DB 841 TCAGGCCACACAGTGA 856
RESULT 11
173428
LOCUS 173428 2405 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 30 from patent US 5686412.
ACCESSION 173428
VERSION 173428.1 GI:3009569
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE Unclassified.
1 (bases 1 to 2405)
AUTHORS Hoeksma,M.F.
TITLE Protein kinases
JOURNAL Patent: US 5686412-A 30 11-NOV-1997;
FEATURES
source
1..2405
/organism="unknown"
BASE COUNT 849 a 392 c 486 g 678 t
ORIGIN

Query Match 48.0%; Score 608.8; DB 6; Length 2405;
Best Local Similarity 71.2%; Pred. No. 6.3e-170;
Matches 880; Conservative 0; Mismatches 337; Indels 19; Gaps 5;

QY 1 atgagccatccttagtagaaagatgaaagacacagacacacacacacacacacacac 60
DB 25 ATGGAATAATAAAGAAAGACAGCAAGCAATACATATGAAATGGCAGCAGCACTAGGT 84


```

QY 329 gtggaaataatgcatggtgctgagctccttgccctagcttgaggagctgtttg 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 571 GCGGAGAGTACAAAGCCATGCTGCTGAGTGTGGGGCCAGCCTTGAGAGCTCTTGC 630
QY 389 acctcttgagcgaacttacttggaagcgtgttaagatgataagcactgctgttc 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 631 ACCTGTGACCGACCTTACGCTCAAGAGGGGTGATGATGCTCATCAGCTGATCA 690
QY 449 ctgaatgagatacgtgcatcacaagaacctattatccagatgltcaagccaagaagat 508
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 691 CCGGCAATGAGTATGTCTACACACAGAGCTAATCTACCGGAGAGTAAACCCGAGACT 750
QY 509 tccctgattgtgcacaagaataagaagacatgttatacacattatgacttggac 568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 751 TCCGTGGGGGCGCCCGGGGACCAAGCGGAGCTGCTGATCCATCATCATGATCGAGGC 810
QY 569 tggccaagagatacatatgaccccgaaacaaacacacacattataggaacacaaa 628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 811 TGGCAAGAGAGTACATGACCCCGAGACCAAGAGCAGATCCGCTACCGGAGACAGA 870
QY 629 gtttaactggaactgacaagataatgtctacaacagcatcttggcaagaagagagcc 688
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 871 GCCTGACGGGACGCGCGCTACATGAGCATCAACAGCAGCACTGGCAAGAGAGAGAGCC 930
QY 689 ggaagagatgattggaagccctgaagccatagttcatatgtattctcttgagagagcc 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 931 GCGCGAGAGCTGAGAGCGCTGGGACACATGTTCAATGATCTCTCTGCGGAGCTTCC 990
QY 749 cctggcaagagactcaagcgtgacacattaaagagagatctcaaaaattggtgagacca 808
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 991 CTTGGCAGGGGCTCAAGGCGGACGCTCAAGAGCGGCTACGAGAAATGAGGGGACACA 1050
QY 809 aaaggaatactccatggaagctctctgtgaaacttccagagagatggaacccacc 868
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1051 AAGCGCGCAAGCCCATGAGAGTGTCTGACAGAACTTCCAGAGAGATGCCACGATACC 1110
QY 869 ttcatatgtcagcgcagctggaacttcttgaaaaaacctgatatgatttcaagacc 928
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1111 TGGCGATGTGCGGCGCTGAGACTTCTCGAAGAGCCGAGCTATGATCTGCGGAGAGC 1170
QY 929 tcttcaagaaccttggaaaagaagagctacacacttgaacttgaactatgattggttg 988
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1171 TCTTACAGGACCTTCTTGACCGGAGTGGCTTCTGTTGAGATGAGATGAGCTGGGCGG 1230
QY 989 ggaagacattactactcagtagggtcagcttcaacgtatgattctgtgcatctgcaataa 1048
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1231 GGAAGCCCCCTGCGGACCCCATCGGACGCTCCAC-----A 1266
QY 1049 ctgagaagaacacacacataagagatcgccatcaacaacagcagccctcttcgaatacagg 1108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1267 CCGAGCTGCGCCTCCAGCCTCAGCTCCGGACAAACCCAGCCGACAGCAACAAACCAAGC 1326
QY 1109 tggtagtctacaacaatggagagctgtgaatgttgatgtccacagggggccacatccaatg 1168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1327 CGTTGAACCTCCACCAAGGGGAGCTGAATCGGAGACCCACGCGCGGCTCCCAAGC 1386
QY 1169 caccacacagagctcagcgcaggtgaggtatgtgaggaagcctaagctgtctgtttct 1228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1387 CCCCAGATCACAGCGCTCGAGAGGTGAGGTGGCGCATGAACCAATGCTGCTTCT 1446
QY 1229 ttaagaagaaagaagaagactgtctcagcgcaagaatga 1269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1447 TCAAGAGAGAGAAAGAAATCGCTCGACGACACAGATGA 1487

```

```

RESULT 13
LOCUS BC020972 2446 bp mRNA linear PRI 22-JAN-2002
DEFINITION Homo sapiens, casein kinase 1, gamma 2, clone MGC:9354
IMAGE:3851613, mRNA, complete cds.
ACCESSION BC020972.1 GI:18088089
VERSION BC020972.1
KEYWORDS MGC.

```

```

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2446)
AUTHORS Strussberg, R.
JOURNAL Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
FEATURES
Source
1..2446
/organism="Homo sapiens"
/db_xref="LocusID:1455"
/db_xref="taxon:9606"
/clone="MGC:9354 IMAGE:3851613"
/tissue_type="Colon, adenocarcinoma"
/clone_id="NIH_MGC_65"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
54..1301
/codon_start=1
/product="casein kinase 1, gamma 2"
/protein_id="AAH20972.1"
/db_xref="GI:18088090"
/translation="MDPDRKGGKGETEGRRMSKAGGSHGINSSTGSSVILWVG
NFRVGRKICGNFGEELRGLNLTNEYVAIKLEPISAPOLHLEFRKQSLAEV
POYVYRPGCNANAMVELLGLSLEDLPOLCRFTLKVLMIAIOLITRMVYTKS
LYRDVYKPEPNLTVRGPRGRHAIHIIIDGLAKVYIDPEYKHIIPYREKSLTGARY
MSINTHLGKEQSRDLEALGHMFMFLNGSLPQGLKADITLKEROKIDPKRRAPL
EVLGNFPEEMATYLVKVRLDPEFEPDYDLRLKLTDLDFDSGFVDFEYDMAGKPL
PPVIGVHDLPSOPLRDRTQPHSKNOALNSTGELNADDEPTAGHSNAPITAPAVE
VADERKCCFFKRRKRSLORHK"
BASE COUNT 518 a 771 c 762 g 395 t
ORIGIN
Query Match 47.5%; Score 603; DB 9; Length 2446;
Best Local Similarity 71.0%; Pred. No. 3,4e-168;
Matches 839; Conservative 0; Mismatches 315; Indels 27; Gaps 2;

```

```

Db 328 TCTCAAGCAGCT---CAGCGCCACAGAGGGCGCTCCCTCAGAGGTCTACTACTTCCGTCGCT
Qy 329 gtgggaataataatgcatggtgtgtgagctccttgccctagcttgaggactgtttg 388
Db 385 GCGGCAATTACAGCCATGTGTGTGAGCTGCTGGGGCCCAAGCTTGAGAGACCTGTTCG 444
Qy 389 acccttgaccgagcaatttcttggaagacggtgttaattatagatcaccagctgtctt 448
Db 445 ACCTGTGCGACCGGACCTTACGCTCAAGACGGTGTGATGATGCCATCCAGCTGATCA 504
Qy 449 ctgcaatggaatgctgactcaagaacatcattacagagatgtaagagcaagagact 508
Db 505 CGGCAATGGAATATGTGACACCAAGAGCCATATCCGGGAGAGTGAAGCCGAGAACT 564
Qy 509 tctgtatgttcgaagaagcaataagaagagcatgttataacattatagacttggac 568
Db 565 TCTGTGTGGGGCGCGCGGAGCCAGCGGAGCATGCTCATCATCATCATCTCGGCG 624
Qy 569 tggcgaaggaatgactgacccgaaacaaacacataccttataagggaacacaaaa 628
Db 625 TGGCAAGGAATATGATGACCCCGACACCAAGACACATCCGCTACCGGAGCACAAGA 684
Qy 629 gtttaactggaactgcaagatataatgtctatacaacacgcatcttggcaagaagacc 688
Db 685 GCGTACAGGGGAGCGCGCGGTACATGAGCATCAACAGCAAGCTGGCAAGAGAGAGCC 744
Qy 689 ggaagatgattggaagccctagaccatgttcatgtatttcttcctgagagcctcc 748
Db 745 GCGCGAGCACTGTGAGCGCGCTGGGCCACATGTTCACTGCTCTCGGCGAGCTTCC 804
Qy 749 cctggaagaagactgaagctggaacacattaaagaagagatatacaaaaattgtgtaccca 808
Db 805 CTTGGCAGGGGCTTAAGGCCGACACGCTCAAGAGCGGTACAGAGATCGGGGACACCA 864
Qy 809 aagaagaaactccatggaagctcctgtggaacatttccagagagagatggaacactca 868
Db 865 AACCGCGACCGCCATGAGAGGTGCTGTGCGAAGCTTCCAGAGAGAGATGGCCACGTAAC 924
Qy 869 ttgcatgttgcagagcgactggaactcttgaaaaaaactgattatgatttaccgacc 928
Db 925 TGCCTATGTGCGCGCGCTGTGACTTCTTCGAGAGCCGAGTATGATGACTGCGGAGAC 984
Qy 929 tcttcaagaagactcttgaagaagaagctacacacttgcctatgctatgattggttg 988
Db 985 TCTTACCGAGACTTGTGACCGCGAGTGGCTTGTGTGACTGATGAGTACGAGCTGGGCG 1044
Qy 989 ggaagactatctactcagtagaggtcagttcagctagatattctgtgcatctgcaataa 1048
Db 1045 GGAAGCCCGTGGCGAGCCCATGCGGACGTCAC-----A 1080
Qy 1049 ctgagaagaagcacaacataagagatcgccatcaacaacagcagcctctcgaataagg 1108
Db 1081 CCGACCTGCGCTCCACGCTCAGCTCCGGGACAAACCCAGCGCACAGCAAAACACAGG 1140
Qy 1109 tggtagtctaaacaaatgagagctgtaattgtatgtatcccaagggggccacatcgaatg 1168
Db 1141 CGTGAAGCTCCACCAAGGGGAGGTGATCGAGACGCCACGCGCGGACACTCCAAAG 1200
Qy 1169 caacaatcagactcagctgagaggtggaaggtagtggaagagcaagtgctgttctt 1228
Db 1201 CCCGATACACAGCGCGCTGCAAGAGTGAAGTGGGCCATGAACCAAAATGCTGCTTCT 1260
Qy 1229 ttaagaggaagaagagactgtctcagcgcaacaagtga 1269
Db 1261 TCAAGAGGAGAAAGAAATCGCTGACGACGACACACAGTGA 1301

```

```

RESULT 14
LOCUS RNU22297 1572 bp mRNA linear ROD 09-JUN-1995
DEFINITION Rattus norvegicus casein kinase 1 gamma 2 isoform mRNA, complete
cds.

```

```

ACCESSION U22297
VERSION U22297.1 GI:854734
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 1572)
AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
          Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
TITLE Casein kinase I gamma subfamily. Molecular cloning, expression, and
          characterization of three mammalian isoforms and complementation of
          defects in the Saccharomyces cerevisiae YCK genes
JOURNAL J Biol. Chem. 270 (21), 12717-12724 (1995)
MEDLINE 95279411
REFERENCE 2 (bases 1 to 1572)
AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
          Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular
          Biology, University of Indiana School of Medicine, 635 Barnhill
          Drive, Indianapolis, IN 46202-5122, USA
FEATURES
     source
         1..1572
            /organism="Rattus norvegicus"
            /db_xref="taxon:10116"
            /note="protein kinase"
            /codon_start=1
            /product="casein kinase 1 gamma 2 isoform"
            /protein_id="AAC52201.1"
            /db_xref="GI:854735"
            /translation="MDPDKGGGGELEEGRMKGTNRNHEVRNCTSSVLNCP
            NFRVGRKICGNGFVRLGKNLYTNEVALKLPISRAPOHLERFYOLSTGVP
            QVYFEGPCRYNAMVELLGPISLEDFLCDRFTLTVMILAIOLTRMEYVHTSL
            IYDVKPENFLVPGSKRSHSIHIDFGIAKEIIPETVKHIIPEYHKSLSLTARYM
            SINTHLGKESDRDLEALGHMVFYRLSPMOGLKADYLKRYOKIGDTKRATPIE
            VICSESPREMATRLRYRLDPEFKPDYDRLFTDLPRSGYVDYEDVMGKPLP
            TPQIVHPDVPSPQPRHDKQHLTKQNALNSTGELNTDDPTFGHSHNAPIAAAEVY
            ADETKCCFFKRRKRSIQRHK"
            1572
     polyA_site
         /note="10 A nucleotides"
BASE COUNT 369 a 475 c 458 g 270 t
ORIGIN
Query Match 45.5%; Score 577.6; DB 10; Length 1572;
Best Local Similarity 70.1%; Pred. No. 1,2e-160;
Matches 819; Conservative 0; Mismatches 319; Indels 30; Gaps 2;

```

Db 594 CACCTTCACGCTAAAGACGGTGTGATGATGCCATCCAGCTCATGATCAGCGCATGAGTA 653
 QY 462 cgtgcatcaagaactcttaccagatgtccaaagcaggaactctctgtatgtcg 521
 Db 654 TGTGCATACCAAGAGCTCTCATCTACCCGAGGTAAAGCTTGAGAACTTCTGTGTGGCG 713
 QY 522 acaagcgaataaagaagatgtttatcatatcatatagatttggatggccaagata 581
 Db 714 GCGGGGACGACAGGAGACACTCCATCCATCATCATGATCTTGGCTGGCCAAAGAGTA 773
 QY 582 cattgaccccgaaacacaaacacatcatatagggaacacaaagtttaacttgaac 641
 Db 774 CATCGACCTTGAGACCAAGAGACATCCGCTACCGGAGACCAAGAGCTGAGCGGAC 833
 QY 642 tgcgaatatatgtctcaacagcactcttgcaagaagacccggagagatgtt 701
 Db 834 GGGGCGCTACATGAGCTCAACAGCAGCTGGGCAAGAGACAGCGCGGCGGAGACT 893
 QY 702 ggaagccctagcagcatatgttcatgtatcttctcgaagcagccctcccttgcagagact 761
 Db 894 GGAAGCGCTAGGGGACACTGTTCATGTACTTCTACGGGGAGTGTGCGCTGGCGAGGCT 953
 QY 762 caaggtgacacatlaaagaagatacaaaaattgtgtgacacaaagaaactacc 821
 Db 954 CAAGCGGACACCGCTCAAGAGACGCTACAGAAAGATTGTGATACAGCGCTGCCAGCGC 1013
 QY 822 cattgaagcctctctgtgaagactctccagagagatgtgcaactacccttgatgtcag 881
 Db 1014 AATCGAGGTCTGTGAGGCTTCCCGAGAGATGGCCACCTACTTGGCTATGTGGC 1073
 QY 882 ggcagtgagactcttctgaaacactgtatagatatttgaagaccccttcccaagact 941
 Db 1074 GCGGCTAGACTTCTTGAAGAGCAGCAGACTAGACTAGCTAGAGAGCTTTCACGACCT 1133
 QY 942 ctltgaaagaaagcgtacacacttgactatgacctatgattgtgtgtggaagactatcc 1001
 Db 1134 CTTCGACCGCAGGCGCTGTTTGTGACTAGATAGTATGAGTGGCGCCGAGCGCCCTGCC 1193
 QY 1002 tactcagatgtgtcagttcagtagatctgtgtcactcgcataactctgagaagca 1061
 Db 1194 GACACCTATGCGACCTCATCTGATGTCCTCCAGCGCCGACATGCTGACA---- 1249
 QY 1062 cacacatagatcgcacacacacagcagcctctctcgaatcagctgtgtgtcagcaac 1121
 Db 1250 -----AAGCTCAGCTCCACACCAACCAACAGCGCTGAACTGCAC 1289
 QY 1122 caatgagagactaatgtgtatgtatccacagagagccactccaatgtcaccaatcacagc 1181
 Db 1290 CAATGGAGAGCTGAACACAGACAGACCCGCGGCGCACTCCACCCCATCGGCGC 1349
 QY 1182 tcatgcagagtgtagtagtagaagtagtgcgtgttcttctaagaggaag 1241
 Db 1350 CCTGCGAAGTAGAGGTGGAGTGAACCAAGTGTGCTGCTTCTTCAAGAGAGGAA 1409
 QY 1242 gaagaagactgtcagcgccacaagtga 1269
 Db 1410 GAGAAATCGCTGACGAGCACTAAGTA 1437
 RESULT 15
 RNU22321 2547 bp mRNA linear ROD 09-JUN-1995
 LOCUS Rattus norvegicus casein kinase 1 gamma 3 isoform mRNA, complete
 DEFINITION cds
 ACCESSION U22321 GI:854736
 VERSION 022321.1
 KEYWORDS Norway rat.
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 2547)

AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
 TITLE Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
 JOURNAL Casein kinase I gamma subfamily. Molecular cloning, expression, and
 MEDLINE characterization of three mammalian isoforms and complementation of
 REFERENCE defects in the Saccharomyces cerevisiae YCK genes
 95279411
 2 (bases 1 to 2547)
 AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
 TITLE Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
 JOURNAL Direct Submision
 Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular
 Biology, University of Indiana School of Medicine, 635 Barnhill
 Drive, Indianapolis, IN 46202-5122, USA
 location/Qualifiers
 FEATURES
 source 1..2547
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 764..2110
 /note="protein kinase"
 /codon_start=1
 /product="casein kinase 1 gamma 3 isoform"
 /protein_id="AAC52202.1"
 /db_xref="GI:854737"
 CDS
 /translation="MDNKKDKDKSDPDRAPSGRSGHSTGTGSSSGVLMVGNFR
 VGKIKGNGEFLRLKNTLYNEYVAIKPEPKSRAPOLHREYKQSGSDGIPQY
 YFPGCKYNAVVELDGLSDLEFDLCRTSLKTYLVAIOLISRMVYSKNTLY
 RYKPEKNTLGRPKNAQOVHTIIDPLGAKVEYIDPEYKHTLSRSHSLTGARVMSI
 NTHLKEQSRDDELALGHEMTFLGSLPMDGLKADTKEXKQIGDKRATPEVL
 CENFPEKMATLYLVARLDLFEKRPDVLKLTPLDLCRGMFPEYEDWIKOLPTP
 VAVOODPALSNREAHQHRDKIQOSKNSADHRAAMSOANPHRLRAHLADRHGG
 SVQVSTGEINTEIDPPTAGRSNAPLTATAEVEMDETKCCFFRRKRTIORRK"
 BASE COUNT 684 a 618 c 628 g 617 t
 ORIGIN
 Query Match 44.6%; Score 566.6; DB 10; Length 2547;
 Best Local Similarity 72.2%; Pred. No. 2,4e-157;
 Matches 766; Conservative 0; Mismatches 289; Indels 6; Gaps 2;
 QY 1 atggaccatcctgtaggaagaagatgaagcaacgaagcaactaaaccatgacaa 60
 Db 764 ATGATTAATTAATAAGAAAGCAAGGACAAATCAGATGACAGATGCGCCAGTGGT 823
 QY 61 aggaagcaacatcgtctgcacatctgtctctatctgcctctgtgtctatgtg 120
 Db 824 CGGTCAAGGCGACACACTTCAGGAACTGG--GTCTTCTCATCTGAGTTTAATGTT 880
 QY 121 ggaacacacttcagaggttggcaagaagatagaatgtgggaactcggagagctcaagta 180
 Db 881 GGAACCTAATCTTGAAGTGGGAAATAATGATGTCGCAATTTGGAGAAATTAACATTA 940
 QY 181 ggtaaaaatctcaacacatgaatgtatgcaatacaaatgtgaacaaataaatacagt 240
 Db 941 GGGAAAAATTTAATACAAATGAATATGTGCGCATTAACATGGAAGCCATGAATCCAGA 1000
 QY 241 gctccacagcttattagagtaacagatttataaacaagcttgcagagtggaagt 300
 Db 1001 GCAACACAGCTGCATTTGGAAATACAGATTCTATTAACAGATTAG---CATGTGAGATGT 1057
 QY 301 ctccacacagtgatattactttggaacatgtgggaataataatgcatgtgtcgaagtc 360
 Db 1058 ATACCTCAAGTTTAACATTTTGGCCCTGTGTGTAATACAAACCTATGGGTGAACTG 1117
 QY 361 ctggccctagcttggaagactctgttgaactctgtgacggaacatttacttgaagag 420
 Db 1118 CTGGAGACTAGTTTGAAGATTGTTGACCTGTGATGAACCATTTTCTCTTAAAC 1177
 QY 421 gtgttaatgatacgaacagcgtcttctcgaatggaatgaatgtcgaacaaagaccc 480
 Db 1178 GTTCTCATGATAGCTATACAGCTGATTTCTCGCATGGAAGTAATCCACTCAAGAACTTG 1237
 QY 481 atttacagagatgtcaagcagaagaacttctgtatgtgtcagaagcaataagaagag 540

```

Db 1238 ATTTACAGAGANTGTAAAGCCGAGAAATTTCTTAATAGAGAGGCGGCAAGAAACAAAGCCGAG 1297
QY 541 catgtataacacatataagacttggacttggccaaggaataacattgaccccgaaaccaa 600
Db 1298 CAGGTGATTCACATCATAGATTGTTGGTTGGCAAGGAATATATGATCCAGAGACAAAG 1357
QY 601 aaacacatacctatagggaacacaaaagttaactggaactggaactgaagatatatgtctatc 660
Db 1358 AAACATATACCATACAGAAACAAAGCCTTACTGAAACAGCCAGATACATGAGACATA 1417
QY 661 aaacgacatcttggcaaaagcgaagcggaagatgatttggaaagccctaggccatatg 720
Db 1418 AACACACATCTTAGAAGAAAGACAGACAGACAGATTTAGAACCTTAGGACATATG 1477
QY 721 ttcatgtatttccttcgaggcagccctcccttggcaaggaactcaaggctgacacattaaa 780
Db 1478 TTCATGTATTTCCTGAGAGGCACTCTTCCTGGCAAGGCGCTAAAGCAGATACATTAAAA 1537
QY 781 gagagatatcaaaaattggtagacccaagaagaatactccattgaagctctctgtgag 840
Db 1538 GAGAGATATCAGAAATGTGAGACACAAACGACACACCGATAGAGAGTGTGTGAA 1597
QY 841 aacttccagagagagatggaaccttaacttcgatatgtcagcggaacttgaactcttga 900
Db 1598 AACTTCCAGAGAAAGAAAGCAACATATCTTCGTTACGTACGAAAGGCTAGATTTTGGAA 1657
QY 901 aaactgattatgattattacggaacctctctacagaaacctcttgaanaaaggctac 960
Db 1658 AAGCCAGACTATGATTACTTAAGAAAGCTTTTACTGACTTGTGTGATGCAAAAGGTAT 1717
QY 961 accttgaactatgacctatgattgggttgggaacctatctcactccagtaagggtcagtt 1020
Db 1718 ATGTTGATTATGAATGATGACTGATGTAACAGTTGCTACTCCTGTAGGTGACGTT 1777
QY 1021 caagtagatcttggtagatctgcaataaactcgagaagcca 1061
Db 1778 CAGCAAGAGCCGGCTCTGTATCGAACAAGAGAACACACCA 1818

```

Search completed: August 17, 2002, 21:26:32
Job time: 3906 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:25:31 ; Search time 207.63 Seconds
(Without alignments)
10493.495 Million cell updates/sec

Title: US-09-765-068-1

Perfect score: 1269
Sequence: 1 atgacactctactagtagga.....ctgtctcagcgccacaaagtga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1269	100.0	1269	22	AAH77991
2	1269	100.0	1269	22	AAH77991
3	1269	100.0	1269	22	AAH77991
4	1267.4	99.9	1267.4	24	AAH77991
5	1213.8	95.7	1213.8	22	AAH77991
6	1144.8	90.2	1144.8	22	AAH77991
7	608.8	48.0	608.8	15	AAH77991
8	608.8	48.0	608.8	15	AAH77991
9	564.8	44.5	564.8	15	AAH77991

10	564.8	44.5	1233	16	AAH77991	Human HRR25-like C
11	501.2	39.5	765	20	AAH77991	Human gene express
12	426.2	33.6	2153	23	AAH77991	Drosophila melanog
13	327.4	25.8	447	20	AAH77991	Human gene express
14	307.8	24.3	1407	20	AAH77991	Human gene express
15	300	23.6	300	20	AAH77991	Human gene express
16	299.8	23.6	1416	21	AAH77991	Arabidopsis thalia
17	291.8	23.0	1374	21	AAH77991	Arabidopsis thalia
18	283.4	22.3	1900	24	AAH77991	Physcomitrella pet
19	280.6	22.1	1116	21	AAH77991	Arabidopsis thalia
20	280.6	22.0	1431	21	AAH77991	Arabidopsis thalia
21	279.6	22.0	3505	15	AAH77991	Protein kinase (CK
22	279.6	22.0	3505	16	AAH77991	Human HRR25-like C
23	279.6	22.0	3505	16	AAH77991	CKI-delta-3Hu isof
24	279.6	22.0	3505	20	AAH77991	Human CKI isoform
25	277.4	21.9	1308	21	AAH77991	Arabidopsis thalia
26	272.6	21.5	1353	21	AAH77991	Arabidopsis thalia
27	271.8	21.4	966	21	AAH77991	Arabidopsis thalia
28	271.8	21.4	1863	21	AAH77991	Arabidopsis thalia
29	271.8	21.4	1865	21	AAH77991	Arabidopsis thalia
30	269.4	21.2	1014	22	AAH77991	Polynucleotide seq
31	268.8	21.2	1617	21	AAH77991	Human prostate can
32	267.8	21.1	1210	15	AAH77991	Protein kinase (CK
33	267.8	21.1	1210	16	AAH77991	Human HRR25-like C
34	267.8	21.1	2914	15	AAH77991	Protein kinase (CK
35	267.8	21.1	2914	16	AAH77991	Human HRR25-like C
36	264.6	20.9	924	21	AAH77991	Arabidopsis thalia
37	263.2	20.7	2033	22	AAH77991	Maize casein kinas
38	262.2	20.7	2468	20	AAH77991	S. pombe CKI Hnpl
39	262.2	20.7	2469	15	AAH77991	Protein kinase (Hh
40	262.2	20.7	2469	16	AAH77991	Schizosaccharomyce
41	261.2	20.6	2019	21	AAH77991	Zea mays DNA fragm
42	258	20.3	1356	21	AAH77991	Mouse CKIepsilon C
43	250.2	19.7	1775	21	AAH77991	Arabidopsis thalia
44	248.6	19.6	1773	21	AAH77991	Arabidopsis thalia
45	245.4	19.3	924	21	AAH77991	Arabidopsis thalia

ALIGNMENTS

RESULT	1
ID	AAH77991 standard; DNA; 1269 BP.
AC	AAH77991.
DT	13-NOV-2001 (first entry)
DE	Nucleotide sequence of human protein kinase SGK248.
XX	Human: protein kinase; cancer; immune disease; cardiovascular disease;
XX	brain disease; neuronal disease; Alzheimer's disease; chromosome 15;
KW	Parkinson's disease; multiple sclerosis; metabolic disorder;
KW	peripheral nervous system disease; amyotrophic lateral sclerosis;
KW	infection; ocular disease; migraine; pain; sexual dysfunction;
KW	mood disorder; attention disorder; cognition disorder; hypotension;
KW	hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	1..1269
FT	/tag- a
FT	/product- "protein kinase"
XX	
XX	MO200166594-A2.
XX	
XX	13-SEP-2001.
XX	
XX	02-MAR-2001; 2001MO-US06838.
XX	
XX	06-MAR-2000; 2000US-0187150.

PR		29-MAR-2000; 2000US-019340A.
PR		13-NOV-2000; 2000US-0247013.
XX		(SUGEN-) SUGEN INC.
PA		
PI		Plozman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX		
DR		PMI: 2001-536777/59.
DR		P-PSTDB; AAG67392.
XX		
PT		Nucleic acids capable of encoding human polypeptides having a kinase or
PT		kinase-like activity, useful for diagnosing a disease selected from
PT		practices, cardiovascular disease and neuronal-associated diseases (e.g.
PT		Alzheimer's disease) -
XX		
PS		Example 1; Fig 1B; 201pp; English.
XX		
CC		The present sequence encodes a human protein kinase. The
CC		gene is located at chromosomal position 15q21.3. The kinase
CC		polypeptides are useful for diagnosing a disease or disorder
CC		selected from cancers (e.g., cancers of tissues and cancers of
CC		hematopoietic origin), immune-related diseases and disorders,
CC		cardiovascular disease, brain or neuronal-associated diseases (e.g.
CC		Alzheimer's disease, Parkinson's disease, multiple sclerosis),
CC		metabolic disorders, peripheral nervous system diseases, amyotrophic
CC		lateral sclerosis, viral infections, infections caused by prions,
CC		infections caused by bacteria, infections caused by fungi, ocular
CC		diseases, migraines, pain, sexual dysfunction, mood disorders,
CC		attention disorders, cognition disorders, hypotension, hypertension,
CC		psychotic disorders, dyskinesias, and organ transplant rejection.
CC		Kinase inhibitors are useful for treating diseases and disorders
CC		described above.
XX		
SQ		Sequence 1269 BP; 390 A; 284 C; 297 G; 298 T; 0 other:
Query Match	100.0%; Score 1269; DB 22; Length 1269;	
Best Local Similarity	100.0%; Pident. No. 0;	
Matches 1269; Conservative	0; Mismatches	0; Indels
		Gaps
OY	1	atgaccacaccttaagtaggaagaaggatgaagaacagcagacaactaaacccattgcacaa
Db	1	atggacacctctctaataaggaaaaggatgaagaacagcagacaactaaacccattgcacaa
OY	61	aggaggtcacacatgctctcgacacatctggtcctcatcgctctcgttggttttataagt
Db	61	aggaggtgcacacatgctctcgacacatctggtcctcatcgctctcgttggttttataagt
OY	121	ggaccaccaacttcaggtgtgcgaagaagatagatgttggaaacttcggagagctcagatta
Db	121	ggaccaccaacttcaggtgtgcgaagaagatagatgttggaaacttcggagagctcagatta
OY	181	ggttaaactctctcaacccaatgaatatgttaacatcaaacctggaaaccaataaatcagct
Db	181	ggttaaactctctcaacccaatgaatatgttaacatcaaacctggaaaccaataaatcagct
OY	241	gtcccaacagcttcattagatagatagattataaacaagcttggcagtcgagtgtaagt
Db	241	gtcccaacagcttcattagatagatagattataaacaagcttggcagtcgagtcgagtgtaagt
OY	301	cctcccaagtgtaattactttggaccacatgttgggaataataatgccaatgttgtgagctc
Db	301	cctcccaagtgtaattactttggaccacatgttgggaataataatgccaatgttgtgagctc
OY	361	cttggcccttaacttggagagactgtttggacctcgtgacccaataattacttgaagcg
Db	361	cttggcccttaacttggagagactgtttggacctcgtgacccaataattacttgaagcg
OY	421	gtgttaattgaagcaccacagctgtcttctcgaatgtgatatcggtcacatcaagaacct
Db	421	gtgttaattgaagcaccacagctgtcttctcgaatgtgatatcggtcacatcaagaacct
OY	481	attaccgaagatgtcaaagccagaagaacttcctgattgtgtgcacaagcatalaagaagag
Db	481	attaccgaagatgtcaaagccagaagaacttcctgattgtgtgcacaagcatalaagaagag

[illegible]

FT /*tag- a
FT /product- "Human kinase protein"
XX
XX MO200153493-A2.
XX
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001MO-US02120.
XX
XX 18-JAN-2000; 2000US-0176690.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Donoho G, Hilbun E, Turner CA, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-442260/47.
XX DR P-PSDB; AAU04636.
XX
XX An isolated nucleic acid molecule encoding a novel human protein useful
PT as therapeutics and to screen libraries isolate clones and prepare
PT cloning and sequencing templates -
XX
XX
XX Claim 1; Page 31; 33pp; English.
XX
XX The sequence represents the coding sequence of a novel human kinase
CC protein. The nucleic acid sequence can be used to screen libraries,
CC isolate clones and prepare cloning and sequencing templates and as
CC hybridisation probes for screening libraries, and as therapeutics such
CC as antisense-therapy and gene-therapy. Probes derived from the DNA
CC or polypeptide sequences can be used in the identification, selection
CC and validation of novel molecular targets for drug discovery.
XX
XX
SQ Sequence 1968 BP; 539 A; 482 C; 473 G; 474 T; 0 other;

Query Match 100.0%; Score 1269; DB 22; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggaccatcctagtaggaagaagatgaagaacggaacgaactaaaccatgagcaaa 60
DB atgaccatcctagtaggaagaagatgaagaacggaacgaactaaaccatgagcaaa 109
QY 61 aggaagtcacacgtctcgcacatcgtctcctcgcacgtcctctggtgttctatggtg 120
DB 110 aggaagtcacacgtctcgcacatcgtctcctcgcacgtcctctggtgttctatggtg 169
QY 121 ggaaccacactcaggtgtgcaagaagatagatgtggaactcgaagagccagatta 180
DB 170 ggaaccacactcaggtgtgcaagaagatagatgtggaactcgaagagccagatta 229
QY 181 ggtaaaaatctacacaaatgaatatgtagcaatcaaatgtgaacaaataaatcagt 240
DB 230 ggtaaaaatctacacaaatgaatatgtagcaatcaaatgtgaacaaataaatcagt 289
QY 241 gctccacagcttatttagtagtagcaatttataaagaagttgagtgagtgaaagt 300
DB 290 gctccacagcttatttagtagtagcaatttataaagaagttgagtgagtgaaagt 349
QY 301 ctccacagagtgattactcttgagcaactgtggaataataatgcagtggtgcgagagtc 360
DB 350 ctccacagagtgattactcttgagcaactgtggaataataatgcagtggtgcgagagtc 409
QY 361 ctggccctagcttggaagacgtgttgacacctgtgacccaacatttacttgaagag 420
DB 410 ctggccctagcttggaagacgtgttgacacctgtgacccaacatttacttgaagag 469
QY 421 ggtgtaattgatacgaacacagcgtcttctcgaatggaataagtgacctcaagaacctc 480
DB 470 ggtgtaattgatacgaacacagcgtcttctcgaatggaataagtgacctcaagaacctc 529
QY 481 attaccgagatgtcaagcaggaacttcctgattgtgcagaagcgaataagaagag 540

DB 530 attaccgagatgtcaagcaggaacttcctgattgtgcagaagcgaataagaagag 589
QY 541 catgttatcacattatagactttggaactgccaaggaataatattgcccgaacaaa 600
DB 590 catgttatcacattatagactttggaactgccaaggaataatattgcccgaacaaa 649
QY 601 aaacacataccttataaggaacacaaaagttaactggaactgcaaatatatactc 660
DB 650 aaacacataccttataaggaacacaaaagttaactggaactgcaaatatatactc 709
QY 661 aaacagcatcttgcaaaagcaaaagccgagagatgattgtgaagccctagagccatag 720
DB 710 aacacagcatcttgcaaaagcaaaagccgagagatgattgtgaagccctagagccatag 769
QY 721 ttcattatcttctcctcgagcagcctccctctgcaaaagactcgaagctgacacattaaa 780
DB 770 ttcattatcttctcctcgagcagcctccctctgcaaaagactcgaagctgacacattaaa 829
QY 781 gagagatcatcaaaaattgtgtgacacaaaggaatactccattggaagctctctgag 840
DB 830 gagagatcatcaaaaattgtgtgacacaaaggaatactccattggaagctctctgag 889
QY 841 aacttcagagagatggaacactccttcgabatgtcaggcgactggaactcttgaa 900
DB 890 aacttcagagagatggaacactccttcgabatgtcaggcgactggaactcttgaa 949
QY 901 aaacggtatattagattttaggaaccccttcacagaactctttgaaagaagagctac 960
DB 950 aaacgttatattagattttaggaaccccttcacagaactctttgaaagaagagctac 1009
QY 961 accttgacatgcctatgattgtgttggaagacctaactccactgagtaggagctt 1020
DB 1010 accttgacatgcctatgattgtgttggaagacctaactccactgagtaggagctt 1069
QY 1021 caagtagattctgtgcatctgcaataactcagagaagaacacacataagagatcgca 1080
DB 1070 caagtagattctgtgcatctgcaataactcagagaagaacacacataagagatcgca 1129
QY 1081 tcacaaagaagcctctcgcgaatcaggtgttagctccaaacaaatgtagagctgaatgt 1140
DB 1130 tcacaaagaagcctctcgcgaatcaggtgttagctccaaacaaatgtagagctgaatgt 1189
QY 1141 gatgatccacggagagccactccaatgacacaaatcagctcatgcccggagtgtagta 1200
DB 1190 gatgatccacggagagccactccaatgacacaaatcagctcatgcccggagtgtagta 1249
QY 1201 gtgaggaagctaaagtgtgttctttaaagagaagaagaagactgtcagagcgc 1260
DB 1250 gtgaggaagctaaagtgtgttctttaaagagaagaagaagactgtcagagcgc 1309
QY 1261 cacaagtga 1269
DB 1310 cacaagtga 1318
DB 1310 cacaagtga 1318
RESULT 3
AA508536 standard; cDNA; 1968 BP.
ID AA508536
XX
XX AA508536;
AC
XX
XX 26-SRP-2001 (first entry)
DT
XX
XX DNA encoding human kinase-like protein.
DE
XX
XX Human; kinase protein; hybridisation probe; therapeutic; gene therapy;
KW antisense-therapy; drug screening; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX MO200153493-A2.
XX

XX Key Location/Qualifiers
FT CDS 370..1638
FT /*tag= a
FT /product= "Human PKIN-10 protein"
XX
XX W0200196547-A2.
XX
XX 20-DEC-2001.
XX
XX 14-JUN-2001; 2001WO-US19444.
XX
XX 15-JUN-2000; 2000US-212073P.
XX 23-JUN-2000; 2000US-213467P.
XX 30-JUN-2000; 2000US-215651P.
XX 07-JUL-2000; 2000US-216605P.
XX 13-JUL-2000; 2000US-218372P.
XX 25-AUG-2000; 2000US-228056P.
XX
XX (INCYTE GENOMICS INC.
XX
XX yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
XX Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DM, Greenwald SR;
XX Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
XX Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
XX Lo TP, Khan F, Recipon SA, Azimzal Y, Policky JJ, Ding L;
XX Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX
XX WPI; 2002-090207/12.
XX P-PSDB; AAE16264.
XX
XX New polypeptides, useful for diagnosing, treating or preventing
XX disorders of growth and development, cardiovascular and lipid, and
XX diseases such as cancer, comprise human kinase polypeptides -
XX
XX
XX Claim 5; Page 183; 197P; English.
XX
XX The invention relates to human kinase PKIN proteins and their
XX corresponding cDNAs. A composition containing PKIN agonist is useful for
XX treating a disease or condition associated with decreased expression of
XX PKIN and a composition comprising PKIN antagonist is useful for treating
XX a disease or condition associated with overexpression of PKIN. The
XX disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
XX myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder
XX (acquired immune deficiency syndrome (AIDS), asthma, Addison's disease,
XX atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
XX autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
XX osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
XX rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
XX bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
XX growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
XX Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio
XX vascular disease (arteriovenous fistula, hypertension, vasculitis,
XX aneurysms, congestive heart failure, angina pectoris, myocarditis,
XX ischaemic heart disease, chronic bronchitis, lung tumours), lipid
XX disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
XX hypercholesterolaemia, obesity). PKIN DNA is useful for assessing
XX toxicity of a test compound and in gene therapy. The present sequence
XX is human PKIN-10 cDNA.
XX
XX Sequence 1689 BP; 495 A; 391 C; 399 G; 404 T; 0 other;
XX
XX Query Match 99.9%; Score 1267.4; DB 24; Length 1689;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 430 aggaagtcacacgtctctgcacacatctgcctccatcgtctcttcttattggtg 489
|||
Qy 121 ggaccacacttcaggtgttgcaagaagaatagatggtggaaacttcgagagcttagatga 180
|||
Db 490 ggaccacacttcaggtgttgcaagaagaatagatggtggaaacttcgagagcttagatga 549
|||
Qy 181 ggtaaatctctacacacaaatgaaatgtagcaatcaaacctggaaacacataaacacgt 240
|||
Db 550 ggtaaatctctacacacaaatgaaatgtagcaatcaaacctggaaacacataaacacgt 609
|||
Qy 241 gtcacacagcttcattagatgagtaacagattataaacagcttggcagtgcaagtgaaagt 300
|||
Db 610 gtcacacagcttcattagatgagtaacagattataaacagcttggcagtgcaagtgaaagt 669
|||
Qy 301 ctccacagtggtatctcttggcaccatggtgggaataataatgccaagtgtctgagctc 360
|||
Db 670 ctccacagtggtatctcttggcaccatggtgggaataataatgccaagtgtctgagctc 729
|||
Qy 361 ctggagccttagcttgagagactgttgacctgtgtgacacgaacatttacttgaagagc 420
|||
Db 730 ctggagccttagcttgagagactgttgacctgtgtgacacgaacatttacttgaagagc 789
|||
Qy 421 ggttaatgtagcaccacagctgtcttctcgaaatggaatagtcgtcactcaagaacctc 480
|||
Db 790 ggttaatgtagcaccacagctgtcttctcgaaatggaatagtcgtcactcaagaacctc 849
|||
Qy 481 attacccagatgtcaagccagagaaactctctgattgtgtcagaagcaataaagaagag 540
|||
Db 850 attacccagatgtcaagccagagaaactctctgattgtgtcagaagcaataaagaagag 909
|||
Qy 541 catgttatcacattatagactgttgactggcgaaggaatacatctggcccggaacccaa 600
|||
Db 910 catgttatcacattatagactgttgactggcgaaggaatacatctggcccggaacccaa 969
|||
Qy 601 aaacacataccttaagggagacacacaaagttaactgtgaactggaactggaatatgtctatc 660
|||
Db 970 aaacacataccttaagggagacacacaaagttaactgtgaactggaactggaatatgtctatc 1029
|||
Qy 661 aacacgcatcttgcaagaagcaagccgagagatgatttggagagcccttgcccatgtg 720
|||
Db 1030 aacacgcatcttgcaagaagcaagccgagagatgatttggagagcccttgcccatgtg 1089
|||
Qy 721 ttctgatttctcttgaggcagctccctcggaaggaactcgaagctggaactttaa 780
|||
Db 1090 ttctgatttctcttgaggcagctccctcggaaggaactcgaagctggaactttaa 1149
|||
Qy 781 gagagatatcaaaaattgtgtgacacacaaaggaatactccatctgaagctctgtgag 840
|||
Db 1150 gagagatatcaaaaattgtgtgacacacaaaggaatactccatctgaagctctgtgag 1209
|||
Qy 841 aacttcagagagagatggaacactccttcgatatgtcagaggaactgactcttgaa 900
|||
Db 1210 aacttcagagagagatggaacactccttcgatatgtcagaggaactgactcttgaa 1269
|||
Qy 901 aaactgattatggtatttaacagacctcttcacagaccttcttgaaagaagagctac 960
|||
Db 1270 aaactgattatggtatttaacagacctcttcacagaccttcttgaaagaagagctac 1329
|||
Qy 961 aacttgactatgctatgattgtgttggaagaccttctcactcaagtgaggtcagtt 1020
|||
Db 1330 aacttgactatgctatgattgtgttggaagaccttctcactcaagtgaggtcagtt 1389
|||
Qy 1021 caagtagattctgtgtcatctgcaataactcagagaagccacacataaggaatcgagcca 1080
|||
Db 1390 caagtagattctgtgtcatctgcaataactcagagaagccacacataaggaatcgagcca 1449
|||
Qy 1081 tcaacaacagagcctcttcgaaatcagagtggtttagcccaacaaatggagagctgaatggt 1140
|||
Db 1450 tcaacaacagagcctcttcgaaatcagagtggtttagcccaacaaatggagagctgaatggt 1509
|||
Qy 1141 gatgatccacagagagccactccaaatgcacacaaatcagactacagctgaggtgaggtga 1200
|||

Db 1510 gatgatcccaagggagcccaactccaaatgcaccaatcacagctcatcgaggtgtagta 1569
QY 1201 gtgaggaagctaaagtctgtcttcttaagagaagaagaagactgctcaagc 1260
|||||
Db 1570 gtgaggaagctaaagtctgtcttcttaagagaagaagaagactgctcaagc 1629
QY 1261 cacaagtga 1269
|||||
Db 1630 cacaagtga 1638
RESULT 5
AAH21501
ID AAH21501 standard; cDNA; 1754 BP.
XX
XX AAH21501;
AC
XX
XX 10-AUG-2001 (first entry)
DE Human casein kinase 48 encoding cDNA SEQ ID NO:1.
XX
XX Human casein kinase 48; cytosolic; immunomodulatory; antiinflammatory;
KW virucide; gene therapy; diagnosis; treatment; malignant tumour;
KW haemopathy; HIV infection; immunological disease; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 199.1515
FT CDS /tag- a
FT /product- "casein kinase 48"
XX
XX WO200129228-A1.
XX
XX PD 26-APR-2001.
XX
XX PE 16-OCT-2000; 2000MO-CN00330.
XX
XX PR 18-OCT-1999; 99CN-0116987.
XX
XX PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
XX
XX PI Mao Y, Xie Y;
XX
XX DR MPI; 2001-282163/29.
XX
XX P-PSDB; AAB97904.
XX
XX PT Human casein kinase 48 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation
XX
XX PS Claim 6; Page 22-23; 30pp; Chinese.
XX
XX CC The present sequence encodes human casein kinase 48 (CK48). CK48 has
CC cytosolic, immunomodulatory, antiinflammatory and virucide activity,
CC and can be used in gene therapy. The CK48 protein and polynucleotide
CC sequences can be used in the diagnosis and treatment of malignant
CC tumour, haemopathy, HIV infection, immunological diseases and various
CC inflammation.
XX
XX SQ Sequence 1754 BP; 536 A; 372 C; 389 G; 457 T; 0 other;
Query Match 95.7%; Score 1213.8; DB 22; Length 1754;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1215; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 atggacatccttagttaggaagaagatgaaagacacagacgaacataaccatgacaca 60
|||||
Db 199 atggacatccttagttaggaagaagatgaaagacacagacgaacataaccatgacaca 258
QY 61 aggaagtcacacgtctctgacatctggtctccatcgtctctctggttcttatgtg 120
|||||

Db 259 aggaagtcacacgtctctgacatctggtctccatcgtctctctggttcttatgtg 318
QY 121 ggacccaactcacaaggttggcagaagaataagatgtgggaacttcggagctcagatta 180
|||||
Db 319 ggacccaactcacaaggttggcagaagaataagatgtgggaacttcggagctcagatta 378
QY 181 ggtaaaaatctcaaccaatgaaatagtagcaatcaaacctggaaccaataaatacagc 240
|||||
Db 379 ggtaaaaatctcaaccaatgaaatagtagcaatcaaacctggaaccaataaatacagc 438
QY 241 gctccacagcttcaatttagatagatattataaacagcttggcagtgagtgagtg 300
|||||
Db 439 gctccacagcttcaatttagatagatattataaacagcttggcagtgagtgagtg 498
QY 301 ctccacagtggtattacttggacacatgtgggaataataatgccaatgtctgagctc 360
|||||
Db 499 ctccacagtggtattacttggacacatgtgggaataataatgccaatgtctgagctc 558
QY 361 ctggccctagcttggagactgttggacctgtgacgtgacggaacattacttgaagacg 420
|||||
Db 559 ctggccctagcttggagactgttggacctgtgacgtgacggaacattacttgaagacg 618
QY 421 gtgttaatgatagcacatcagctcttctcgaatggaatacgtgcactcaaaagctc 480
|||||
Db 619 gtgttaatgatagcacatcagctcttctcgaatggaatacgtgcactcaaaagctc 678
QY 481 attaccagatgtcacaagccagagaactcctgtattgtgacagaagcaataagaagag 540
|||||
Db 679 attaccagatgtcacaagccagagaactcctgtattgtgacagaagcaataagaagag 738
QY 541 catgtatcacatataagacttggactggcgaaggaatacatgtgacccgaaacaaa 600
|||||
Db 739 catgtatcacatataagacttggactggcgaaggaatacatgtgacccgaaacaaa 798
QY 601 aaacacataccttataggaacacaaaagttaactggaactggaatgaatatatgtcattc 660
|||||
Db 799 aaacacataccttataggaacacaaaagttaactggaactggaatgaatatatgtcattc 858
QY 661 aacacgactcttggcagaagcagaagccggagagatgttggagccctagggcattg 720
|||||
Db 859 aacacgactcttggcagaagcagaagccggagagatgttggagccctagggcattg 918
QY 721 ttcatgattccttcgaggaagcctccctggaaggaactcaagcttgacacattaaa 780
|||||
Db 919 ttcatgattccttcgaggaagcctccctggaaggaactcaagcttgacacattaaa 978
QY 781 gagagatatcaaaaatgtgtgacacacaaaaggaatactccattgaagctctctgtgag 840
|||||
Db 979 gagagatatcaaaaatgtgtgacacacaaaaggaatactccattgaagctctctgtgag 1038
QY 841 aacttcagaagagatggcgaacctcctcgatatgtcagaggcgactggactcttgaa 900
|||||
Db 1039 aacttcagaagagatggcgaacctcctcgatatgtcagaggcgactggactcttgaa 1098
QY 901 aaacctgattatggaatttaacggaccccttcacaacacctcttgaagaagaagctac 960
|||||
Db 1099 aaacctgattatggaatttaacggaccccttcacaacacctcttgaagaagaagctac 1158
QY 961 accttgaactatgctatgttgggtgtggagaccttctcactcaagtaggtcaggt 1020
|||||
Db 1159 accttgaactatgctatgttgggtgtggagaccttctcactcaagtaggtcaggt 1218
QY 1021 cacgtaatctgtgtgcatctgcacataactcgagaagaagccacacataagagatcgcca 1080
|||||
Db 1219 cacgtaatctgtgtgcatctgcacataactcgagaagaagccacacataagagatcgcca 1278
QY 1081 tcacaacagagacctcttcgaatcaggtgttagctcaaccaaagtgaagctgtatgtt 1140
|||||
Db 1279 tcacaacagagacctcttcgaatcaggtgttagctcaaccaaagtgaagctgtatgtt 1338
QY 1141 gatgatcccaagggagccactccaatgacccaatcacaagctcatgcccaggtgtgaggtta 1200
|||||
Db 1339 gatgatcccaagggagccactccaatgacccaatcacaagctcatgcccaggtgtgaggtta 1398

QY 1201 gtgaggagactaatg 1217
|
Db 1399 gtgaggagactaatg 1415

RESULT 6
AAH78262
ID AAH78262 standard; cDNA; 4417 BP.
XX
AC AAH78262;
XX
DT 26-NOV-2001 (first entry)
XX
DE Nucleotide sequence of human kinase 15977.
XX
XX Human; kinase; 2504; 15977; 14760; cellular proliferative disorder;
KM cellular differentiative disorder; neural disorder; immune disorder;
KM cardiovascular disorder; liver disorder; skin disorder;
KM skeletal muscle disorder; bone metabolism; cardiovascular disorder;
KM viral disease; pain; metabolic disorder; blood vessel disorder;
KM hepatic disorder; liver disorder; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 337..1716
FT /*tag= a
FT /product= "Kinase"
XX
XX WO200164905-A2.
XX
XX 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US06525.
XX
XX 29-FEB-2000; 2000US-0186061.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Olant PJ, Kapeller-Libermann R, Meyers RA;
XX
XX WPI; 2001-570697/64.
XX
XX P-PSDB; AAG67542.
XX
XX New protein kinase family polypeptides for treating hematopoietic
PT neoplastic disorders, immune disorders, cardiovascular disorders and
PT disorders of blood vessels
XX
XX Claim 2; Fig 4A-C; 145pp; English.
XX
XX The present sequence encodes human kinase 15977. The specification
CC also describes kinases 2504 and 14760. The kinase polypeptides and
CC polynucleotides are used to treat cellular proliferative or
CC differentiative disorders, neural disorders, immune disorders,
CC cardiovascular disorders, liver disorders, skin disorders and skeletal
CC muscle disorders. They may also be used for controlling disorders
CC associated with bone metabolism, cardiovascular disorders, viral
CC diseases, pain or metabolic disorders, blood vessel
CC disorders, and hepatic or liver disorders.
XX
XX
SQ Sequence 4417 BP; 1240 A; 1006 C; 1066 G; 1105 T; 0 other;

Query Match 90.2%; Score 1144.8; DB 22; Length 4417;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1267; Conservative 0; Mismatches 2; Indels 111; Gaps 1;

QY 1 atggaccatcctagtaggaagaagatgaagaacagcgaacactaacatgacaa 60
|
Db 337 atggaccatcctagtaggaagaagatgaagaacagcgaacactaacatgacaa 396
|
QY 61 aggaagtacacacgtctctgcacacatctgctctccatcgcctctggttctatggtg 120

Db 397 aggaagtacacacgtctctgcacacatctgctctccatcgcctctggttctatggtg 456
|
QY 121 ggaaccaactcgaaggttggcaagaagatagatgtgggaacttcggaagcccaatta 100
|
Db 457 ggaaccaactcgaaggttggcaagaagatagatgtgggaacttcggaagcccaatta 516
|
QY 181 ggtaaaaatctacaccaatgatatgtatgacaactgaactggaacaaataacacgt 240
|
Db 517 ggtaaaaatctacaccaatgatatgtatgacaactgaactggaacaaataacacgt 576
|
QY 241 gctccacagcttcatttagatagatcagaatttataaacaagcttggcagtggaagtgag 300
|
Db 577 gctccacagcttcatttagatagatcagaatttataaacaagcttggcagtggaagtgag 636
|
QY 301 ctcccaacagtgtaactacttggacacatgtgggaataataatgcattggtcggaactc 360
|
Db 637 ctcccaacagtgtaactacttggacacatgtgggaataataatgcattggtcggaactc 696
|
QY 361 ctggccctagcttggagacgttggtaacctctgtgacccaattacttgaagacg 420
|
Db 697 ctggccctagcttggagacgttggtaacctctgtgacccaattacttgaagacg 756
|
QY 421 gtgttaatgatacgaatccagctgcttctcgaatggaatacgtgcactcaagaacctc 480
|
Db 757 gtgttaatgatacgaatccagctgcttctcgaatggaatacgtgcactcaagaacctc 816
|
QY 481 attaccgaagatgcaagccagaagaacttcctgattgtgtgcagaagccaataagaag 540
|
Db 817 attaccgaagatgcaagccagaagaacttcctgattgtgtgcagaagccaataagaag 876
|
QY 541 catgtatacacattataagcttggagctggccaagaataacattgcccgaacaa 600
|
Db 877 catgtatacacattataagcttggagctggccaagaataacattgcccgaacaa 936
|
QY 601 aaacacataccttataaggaacacaagaatttaacttgaactgcgaataatgtctatc 660
|
Db 937 aaacacataccttataaggaacacaagaatttaacttgaactgcgaataatgtctatc 996
|
QY 661 aacacgacatctggcaagaagcaagccgagagatgattggagccctagccatag 720
|
Db 997 aacacgacatctggcaagaagcaagccgagagatgattggagccctagccatag 1056
|
QY 721 ttcatgtatttctctcgaagcagctccctcctggaagaagctcaaggttgacattaaa 780
|
Db 1057 ttcatgtatttctctcgaagcagctccctcctggaagaagctcaaggttgacattaaa 1116
|
QY 781 gagagatatcaaaaattgtgtgacccaagaagatctccattggaagctctgtgag 840
|
Db 1117 gagagatatcaaaaattgtgtgacccaagaagatctccattggaagctctgtgag 1176
|
QY 841 aacttccagagagatggaacactccttcgatatgtcaggcggaactggaactcttggaa 900
|
Db 1177 aacttccagagagatggaacactccttcgatatgtcaggcggaactggaactcttggaa 1236
|
QY 901 aaacgtgattatgattttagcgaaccttccacaacctcttggaaaagaaggttac 960
|
Db 1237 aaacgtgattatgattttagcgaaccttccacaacctcttggaaaagaaggttac 1296
|
QY 961 accttgaactgcctatgattgtgtgtggagacctatctcactcaagttaggtcagtt 1020
|
Db 1297 accttgaactgcctatgattgtgtgtggagacctatctcactcaagttaggtcagtt 1356
|
QY 1021 cactgtagattctgtgcatctgcaataactcgaagaagccacacataaggaatcgcca 1080
|
Db 1357 cactgtagattctgtgcatctgcaataactcgaagaagccacacataaggaatcgcca 1416
|
QY 1081 tcacaaagcagcctctctggaat----- 1104
|
Db 1417 tcacaaagcagcctctctggaatlcagaatgtatcatcagaagcgccgagagagtgga 1476
|
QY 1105 ----- 1104

Db 919 aaacagactatgactacttaagaagcttttactgactgtttgtatcgaaagatat 978
QY 961 acccttgactatgctctgtgtgtgtggaagccttctctctccagtaggtcagt 1020
Db 979 atgttattatgaatgatgtgattgtaaacagtttgcctactcactcagtggtcagt 1038
QY 1021 cagctgattctgtgtgactgataaactcaggaagcacaataagagtcgcga 1080
Db 1039 cagcaagatctgtctgtcattcaataca---gagaagcaatacaatacagaagatg 1095
QY 1081 tcacaagaagcagcctcttcgaatcaggtgttagctcaacccaatggagagctgaatgt 1140
Db 1096 caacacaccca-----aaaccagttgttaagttctataaagagagtaaacaca 1146
QY 1141 gatgattccacggagagccactcactcagcaccatcactcagtcagggagagta 1200
Db 1147 gatgaccccccagcag-acgttcaaatgacacccatcacacccctactgaagtagaagt 1205
QY 1201 gtgaggaagctaaagtgtgtgttcttctaagag 1236
Db 1206 atggaatgaacacactgcagaaagtgtgaacatg 1241

RESULT 8
AAQ92962
ID AAQ92962 standard; DNA; 2405 BP.
XX
AC AAQ92962;
XX
DT 25-JAN-1996 (first entry)
XX
DE Human HRR25-like casein-kinase-I CKI-gamma-1Hu gene.
XX
XX Casein-kinase-I; HRR25; protein-tyrosine-kinase; CKI-gamma-1Hu;
KW protein-serine/threonine-kinase; enzyme; DNA repair;
KM DNA recombination; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 67..1197
FT CDS /tag= a
XX
PN MO9519993-A1.
XX
PD 27-JUL-1995.
XX
PF 23-JAN-1995; 95WO-US00955.
XX
PR 21-JAN-1994; 94US-0185359.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Hoekstra MF;
XX
DR WPI: 1995-269419/35.
XX
DR P-PSDB; AAR76625.
XX
PT New monoclonal antibodies against human casein Kinase Class I
PT enzymes - useful for purificn. and determ. of these enzymes and to
PT modulate their receptor -ligand binding, also new hybridomas
XX
PS Disclosure; Page 100; 125bp; English.
XX
XX This human casein-kinase-I (CKI-gamma-1Hu) gene which is a homolog
CC of a DNA recombination and repair gene called HRR25 (HO and/or
CC radiation repair) possesses both protein-tyrosine-kinase and protein
CC serine/tyrosine-kinase activities. HRR25 operates to promote repair
CC of DNA strand breaks at a specific nucleotide sequence and is the
CC only protein-kinase known to have such recombination/repair
CC promoting activity. DNA encoding HRR25 can be used to isolate and
CC identify related sequences, while recombinant HRR25, or cells
CC expressing it, can be used to screen compounds for their effects

CC on DNA repair and kinase activities.
XX
SQ Sequence 2405 BP; 849 A; 392 C; 486 G; 678 T; 0 other;
Query Match 48.0%; Score 608.8; DB 16; Length 2405;
Best Local Similarity 71.2%; Pred. No. 1.3e-180;
Matches 880; Conservative 0; Mismatches 337; Indels 19; Gaps 5;
QY 1 atgaccatccttagttaggaagaagatgaaagacagcagcaataacccatgacaa 60
Db 25 atggaataataaagaagaagacaggaacaaatcagatgatactgacagcactagtgt 84
QY 61 aggaatgcacactgctcgcacccatcgtgcctccctcgttcctgttcttattgtg 120
Db 85 cgatcggaacacacactcaggaagactggtcttcacg---ctgagtttaattggtt 141
QY 121 ggaaccacttcagggtgtgcaagaagatagatgtagtggaaactcggagagtcagata 180
Db 142 ggaacttaactttagagttggaataaaatggatgtagtgcattttggagatttcgatta 201
QY 181 ggtaaaaatctacaccaaataatgtagcaatcaactggaaaccaataaacagt 240
Db 202 gggaaaaatttatacacaagaatgatatgtgtgcaattagttggagcccatgaaatcaaga 261
QY 241 gctccacagtttaatttagatgacagatttatataaagcttgcagtgagtggaagt 300
Db 262 gcaacaaagtacatttggatacagaatcctataagcagttag--gactggagatggt 318
QY 301 ctcccaaggtgtaattacttgcagccatgtggaataataataatgacatgctgtgagctc 360
Db 319 ataccctaaatttactatcttcgcgcctgtggtataataacatgatagtgtcgtgaactg 378
QY 361 ctggccctagcttggagagactgttgcacctcgtgacccgaacatttacttgaagag 420
Db 379 ctggacactagtttggagagactgttgcactgtgtgacagaaacatttctcttaaaaa 438
QY 421 gtgttaatgtaacacacacagctgcttctcgaatgtaacgtaacgtaacaaagactc 480
Db 439 gtctcatgatacgaacacacacagcttctcgaatgtaacgtaacgtaacaaagactc 498
QY 481 attacagagatgcgaagcaggaacttccgtatgtgtgcacaagcaataagaagaag 540
Db 499 atatacagaagatgtaaacctgtgaacttcttaataagacgacggaacaaacacccag 558
QY 541 catgttatcacatataagacttgcactgtgccaaggaataacattgaccccgaaacaa 600
Db 559 caagtattcacattatgatttgtgtgcgaaggaataatattgtccggagacaag 618
QY 601 aaacacatccttatagggaacacaaagtttaactgtgaactgcaagatatagtctatc 660
Db 619 aaacacatacatalacaggaacacaaagccttacaggaacacatagatatagaagata 678
QY 661 aacacgactctggcaaaagcgaagcggagagatgattgtggaagccctcagcagcatg 720
Db 679 aacacacatttaggaagaagacaaagtagaagagcatttagaaggttcagtcatatg 738
QY 721 ttcattatttcttcgaagcagcctccctggcaaggaactcgaagctgacacattaaa 780
Db 739 ttcattatttcttcgaagcagccttccttcgtgcaagccttaagagctgacacattaa 798
QY 781 gagaagatataaaaattgtgtgacacaaagaataactccattagagctctctgag 840
Db 799 gagaagatataaaaattgtgtgacacaaagaataactccattagagctctctgag 858
QY 841 aacttcagagagatgtggaacctcactcgtatgtgcggagcagcagctcttgaa 900
Db 859 aatttccagaagaataatgaaacatatcttcgttatgtaagaagcagctcttttttga 918
QY 901 aaactgattatgattatgcagaccttccacagacactcttggaaaagaagagctac 960
Db 919 aaaccagactatgactacttaagaagcttttactgactgtgtgtgtgcgaagaagtat 978

QY 961 accttgactatgctatgattggttgagagacctatctactcagtaggtagcagt 1020
 Db 979 atgttgatttgatgatactgattggttaacagcttccactcagtggtcagct 1038
 QY 1021 cagtagatttctgtgctcgcataactcgcagaagaacacacacatagatgcga 1080
 Db 1039 cagcaagatcctgctcgtctcatcaaca--gagaagacatcaacacagagataatg 1095
 QY 1081 tcacacagcagcctcttcgaatcaggttggttagctcaacaaatgagagctgattgt 1140
 Db 1096 caacatccaa-----aaaccaggttgtagttcttaacaatgagagtagtaacaca 1146
 QY 1141 gatgatccacgagagagccactcaatgcacacacagctcatgcccaggtgagga 1200
 Db 1147 gatgacccacgcag--acgttcaaatgcaccatcacagccctactcagtagaagt 1205
 QY 1201 gtgaggaagcgttaagtgtctgttctttaagag 1236
 Db 1206 atggatgaacacacacgcagaaagtgttgacatg 1241

RESULT 9

AA070828
 ID AA070828 standard; cDNA; 1233 BP.

XX AC AA070828;

XX DT 17-MAR-1995 (first entry)

XX DE Protein kinase (CKIgamma2Hu) coding sequence.

XX KM Protein kinase; immunogen; antibody; protein-tyrosine kinase;

XX KM Protein-serine/threonine kinase; recombination; repair; screening;

XX OS detection; casein kinase; ss.

XX OS Homo sapiens.

XX FX Key Location/Qualifiers

XX FT CDS 1..1044

XX FT /*tag- a

XX FT /product= Protein kinase.

XX PN W09417189-A.

XX PD 04-AUG-1994.

XX PE 21-JAN-1994; 94MO-US00795.

XX PR 21-JAN-1993; 93US-0008001.

XX PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX PI Hoekstra MF;

XX XX WPI; 1994-264102/32.

XX DR P-PSDB; AAR56530.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

CC protein possesses both protein-tyrosine kinase and
 CC protein-serine/threonine kinase activities. Also, HRR25 operates to
 CC promote repair of DNA strand breaks at a specific nucleotide sequence
 CC and is the only protein kinase known to have such
 CC recombination/repair promoting activity. Recombinant HRR25-like
 CC proteins and host cells expressing them are useful in screening
 CC methods designed to examine the effects of various compositions on
 CC DNA break repair and protein kinase activities of the protein. The
 CC HRR25-like proteins are casein kinase class I protein kinases.
 CC XX
 SQ Sequence 1233 BP; 432 A; 214 C; 260 G; 327 T; 0 other;

Query Match 44.5%; Score 564.8; DB 15; Length 1233;
 Best Local Similarity 72.7%; Pred. No. 6,16-167;
 Matches 803; Conservative 0; Mismatches 282; Indels 19; Gaps 5;

QY 133 aggttgcaagaagatgagatggtgagagctcggagagctcagattgtaaaaatc 192
 Db 1 agagtggaaaaaaatgagatggtgcaatttggagattacgattagggaaaaattla 60
 QY 193 tacacccaatgatatgtagcaatccaactggaacccaataaatacagtcaccacagctt 252
 Db 61 tacacaatgataatggtgcaatcaatgagtcgacccaatgaatcaagaacacacagcta 120
 QY 253 cattagagtagcagatttataaacaagcttgcagtgaggtggaaggtccccaaggtg 312
 Db 121 catttgatatacagattctataacagcagttag--gattcggatgtagtatacccaagtt 177
 QY 313 tattacttggacaatggtggaataataatgcattggtgtgtgagctccttgccctagc 372
 Db 178 tactattcggcccttggtaataataacatgctatgtgtcgtgagctctggtgacctgt 237
 QY 373 ttgagagactgtgtgagactctgagacgaacatttattggaagacggtttatagta 432
 Db 238 ttggaagactgtgtgagactctgagacgaacatttctcttaaacagtcctcatgata 297
 QY 433 gccatccagctgcttcttcgaatgtaacgctgacacaaacacacacacacacacac 492
 Db 298 gctatacaactgattcttcgcagatgtaattgcatcctaagaacacttgatatacagagat 357
 QY 493 gtcaagcagaagaactctcgtatgtgtcgcagaagcaataagaagaagatgtatatcac 552
 Db 358 gtaaacctggaactcttcttataagacacgaagaaacacacccagcaagttatcac 417
 QY 553 attatgacttggacgtgcaagaagatgacattgaccccggaacacaaacacacacacac 612
 Db 418 attatgacttggatgtgcaagaagatgacattgaccccggaacacaaacacacacacac 477
 QY 613 tataggaacacaaagttaactggaactgcaagatatgctatcaacacagcattct 672
 Db 478 tacagagaacacaaagagccttacaggaacagctagatatgagcatataacacacattla 537
 QY 673 ggcacaagacaaagccgagagatgattggaagcccttaggcacatagtctattctc 732
 Db 538 ggaaaaagaacaaagtagaagagacgattagaacgtttagatcattgattatgatt 597
 QY 733 cttagaggaagcctcccttcgcaagagactcaaggtctgacacattaaagaagagatcaa 792
 Db 598 ctgagaggaagcctcccttcgcaagagactcaaggtctgacacattaaagaagagatcaa 657
 QY 793 aaaattggtgacacaaagaagatataccatccatgaaactcctctgtggaacttccagag 852
 Db 658 aaaattggaagtaacaaagcggtacacacacatagaagtgtatgtgaaatttccaa--- 714
 QY 853 gagatggcaactcctctgatatgtaagagcagactgagactccttgaaaacccgattat 912
 Db 715 gaaatggcaacatattctgtttagtaagaggtctatatttttggaaaaacccagactat 774
 QY 913 gagatttaggaccccttcacagacactcttgaagaagaaggtcacacttgactat 972
 Db 775 gactacttaagaagccttttactgacttgttgcatagaagaagatatattgttgatatt 834

QY	973	gcatatgatgtgggttggagacctattctactccagtggtgactgaatattct	1032
Db	835	gaatatgcttgatgtgttaaacagatttgcctactccagttgggtgcagtttcagaagaatct	894
QY	1033	ggtgatcttgcataactctgagaagccacacacataagggatcgcgcctaccacaagaacag	1092
Db	895	gctctgtatcatcaaca--gagaagcacacacacacagagataagttgcacaacatccaa-	950
QY	1093	cctcttgcgaatcagtggtttagctcaaccaatcggagagctgaattgtatgatccacg	1152
Db	951	-----aaaccgggttgaagtcttaccacaatggagagattaaacacagatgaccccaac	1002
QY	1153	ggagccaccatccaatgcacacatcacagctcatcgtccaggtggaggtagtggagaagct	1212
Db	1003	gcag-acgttcaaatgtgacacatccacagccctactcgaagtgaagttgatgtgaac	1061
QY	1213	aagtgcgcgtgttctcttaagag	1236
Db	1062	aactgcagaaaggttgaacatc	1085
	RESULT 10		
	AAQ92963		
ID	AAQ92963	standard; cDNA; 1233 BP.	
XX	AC		
XX	AAQ92963;		
DT	25-JAN-1996	(first entry)	
XX			
DE	Human HRR25-like casein-kinase-I CK1-gamma-2Hu gene.		
XX			
KW	Casein-kinase-I; HRR25; protein-tyrosine-kinase; CK1-gamma-2Hu;		
KM	protein-serine/threonine-kinase; enzyme; DNA repair;		
KW	DNA recombination; ss.		
XX			
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
XX	CDS	1..1041	
XX	FT	/*tag- a	
XX	W09519993-A1.		
XX			
PD	27-JUL-1995.		
XX			
PF	23-JAN-1995; 95MO-US00955.		
XX			
PR	21-JAN-1994; 94US-0185359.		
XX			
PA	(SALK) SALK INST BIOLOGICAL STUDIES.		
XX			
PI	Hoekstra MF;		
XX			
DR	WPI; 1995-269419/35.		
XX	P-PSDB; AAR/6626.		
XX			
PT	New monoclonal antibodies against human casein Kinase class I		
PT	enzymes - useful for pulfien, and determ. of these enzymes and to		
PT	modulate their receptor -ligand binding, also new hybridomas		
XX			
XX	Disclosure; Page 104; 125pp; English.		
XX			
XX	This human casein-kinase-I (CKI-gamma-2Hu) gene which is a homolog		
CC	of a DNA recombination and repair gene called HRR25 (HO and/or		
CC	radiation repair) possesses both protein-tyrosine-kinase and protein		
CC	serine/tyrosine-kinase activities. HRR25 operates to promote repair		
CC	of DNA strand breaks at a specific nucleotide sequence and is the		
CC	only protein-kinase known to have such recombination/repair		
CC	promoting activity. DNA encoding HRR25 can be used to isolate and		
CC	identify related sequences, while recombinant HRR25, or cells		
CC	expressing it, can be used to screen compounds for their effects		
CC	on DNA repair and kinase activities.		
XX			

Seq	Sequence	1233 BP; 432 A; 214 C; 260 G; 327 T; 0 other:
Query Match	44.5%; Score 564.8; DB 16; Length 1233;	
Best Local Similarity	72.7%; Pred. No. 6, 1e-167;	
Matches	803; Conservative 0; Mismatches 282; Indels 19; Gaps	
QY	133 agggctgcgaagaagatagatctgtggaaccttcggagagcctcagattggtataaaatc	192
DB	1 agagctgtaaaaaaattggtatgctggaattcttggaattcggatcagattcgtggaaaaattca	60
QY	193 taacccaatgatattgtagcaatcaactcggaaacccaataaatacgcgtgtcccaagctt	252
DB	61 taccacaatgatattgtggaattaaagtcttgagcccaatgaataatcaagagcaccacaagcta	120
QY	253 catttagatgacaatttataaaccgcttgcagatgcagatgcgaaggtctcccaagctg	312
DB	121 catttggaaatcagatctctataagcagttag---gactcggagatggtatatacctaagct	177
QY	313 tatiactcttgacacatgttggnaaataabaatgcabattgctgagctcccttgcctcagc	372
DB	178 tactatttcgcgccttctgtgtaataacaatgcatatgctgtatgtaactcgtgcagatagt	237
QY	373 ttgagagacttgtttgacccctctgtgacccaacttactcttgaagaagcgtgtatagta	432
DB	238 ttggaagactctgtttgactctgttgcgaagaacacttctccttaaaacagcttccatgcta	297
QY	433 ggcactccagcgtgcttcttcgaatggaaatacgtgcacttaaaagaacctcatccagagat	492
DB	298 gctatacaactcgattctctgcgatggaaatagtccatctcaataaagaacttgatataacagagat	357
QY	493 gtcaagccagaagaactctctcgtattgtgtcgacaagaagccaataagaagatgatatcac	552
DB	358 gtaaaacctggaactcttctaataagagccagcaagaacaaaccgaagttttttcac	417
QY	553 attatagactttgacatgcgcgaagaagataacattgaccccgaaacccaanaaacatctact	612
DB	418 attatagatttttctgttcttggaanaagaaatataatgtaacgcgagacaaagaataacatacca	477
QY	613 tataagggaacaaaagaatttaactggaactgcgaagatafatgtctatacaacacgacatctt	672
DB	478 taccgagacaccaaagagccttaccagbaacgcgtagtatatgagcabaacacacattta	537
QY	673 ggcacaagaacaaagccgagagagatgatttggaaagccctcggccatacgttcatgtattcc	732
DB	538 ggaaaagacaagaagtagaagaagacgatttagaagcttttagcatatgttcaigtatttt	597
QY	733 ctgcgaagcagcctccctctgycgaagactcaagatgcctgcacacatttaagaagagatatcaa	792
DB	598 ctgagagacactctctcctcttgcaagcgtcttaaaagtttgcacacattaaagagaggtatag	657
QY	793 aaatatgttgcacacaaaagaagaaatcccatctggaagcgtctcctgcgagaacttccagag	852
DB	658 aaatatgtgagatacaaaaacgggtaccaccaatagaagtttatgtggaanaattttcca---	714
QY	853 gagaatggaacctacactctgcgatatgttccagcgagactggaactctcttggaaaaacctgatat	912
DB	715 gaatatggaacatactcttcgttgttaagaagcctagatttttttggaaaaaccagaactat	774
QY	913 gagtatttaaggacctctctcaacagacactttttgaaaagaagaagcttacaacctttgacctat	972
DB	775 gactacttaagaagaagccttttactgactatcttcttgtaacgcgaanaagagatatgttttatat	834
QY	973 ggcctatgttgggttgggagagaccattctcactccagatgggttgcagttcaagtatgattct	1032
DB	835 gaatatgctcgtgattgtgttaaacagttgctcattcccaacggtgggtgcagcttcagagaagatct	894
QY	1033 ggtgcatctgcgaataactcgaagaagccacacacataaggatctggccatcacacaacagag	1092
DB	895 gctctgtcatcaaca---gagaagacacatcaacacagagataagatgcaacaatccaa-	950
QY	1093 cctcttcgaatacaggtgtgttagctcaacaaatgagagagctgaatgttgatattcccaag	1152

Db 951 -----aaaccaggtgttaagttctacaatgtgagaggttaaacacagatgacccacc 1002
 Qy 1153 ggaaccacatccaatgacacacacacagatgagaggtgtgagaggaagct 1212
 Db 1003 gcaag-acgttcaaatgacacacacacagacccctactgtagtgaagtgtgatgaacc 1061
 Qy 1213 aagtgctgtctgttcttctaagagg 1236
 Db 1062 aactgcacagaaagtgtgaacatg 1085

RESULT 11
 ID ABL16390 standard; cDNA: 765 BP.
 AC ABL16390;
 DT 12-Oct-1999 (first entry)

DE Human gene expression product cDNA sequence SEQ ID NO:3860.
 KW Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer;
 KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
 OS Homo sapiens.
 PN MO9938972-A2.
 PD 05-AUG-1999.
 PE 28-JAN-1999; 99WO-US01619.
 PR 03-APR-1998; 98US-0080666.
 PR 28-JAN-1998; 98US-0072910.
 PR 24-FEB-1998; 98US-0075954.
 PR 31-MAR-1998; 98US-0080114.
 PR 03-APR-1998; 98US-0080515.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 PI Crivenjakov R, Dickson M, Drmanac S;
 PI Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
 PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
 PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
 PI Stache-Crain B, Suduth-Klinger J, Williams LT;
 WP: 1999-494092/41.
 DR 1999-494092/41.
 XX Novel human genes and their expression products which are
 PT differentially expressed in different cell types
 PS Claim 1; Page 1835; 2479pp; English.

CC The present invention describes a library of human polynucleotides
 CC comprising the sequences given in ABL12532 to ABL1779. Also described is
 CC a method of detecting differentially expressed genes correlated with the
 CC cancerous state of a mammalian cell, comprising detecting at least one
 CC differentially expressed gene-product in a test sample from a cell
 CC suspected of being cancerous, where the gene product is encoded by one
 CC of the 5248 polynucleotide sequences given in ABL12532 to ABL1779. The
 CC polynucleotides can be used as a source of primers and probes, which can
 CC be used for a variety of purpose, e.g. detection of expression levels,
 CC mapping, tissue typing or profiling, forensic, genetic analysis and
 CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
 CC can be used for raising antibodies for experimental, diagnostic and
 CC therapeutic purposes. The polynucleotides may also be used to construct
 CC arrays for diagnostics (which may be used to determine function of an
 CC encoded protein); and to detect differences in expression levels between
 CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
 CC identify a genetic predisposition or susceptibility to a disease such as
 CC cancer). The polynucleotides of the invention are especially used in the

CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
 CC and lung cancer. The polynucleotides can also be used to screen for
 CC peptide analogues and antagonists.
 CC Sequence 765 BP; 221 A; 177 C; 173 G; 184 T; 10 other;
 SO

Query Match 39.5%; Score 501.2; DB 20; Length 765;
 Best Local Similarity 99.4%; Pred. No. 4.8e-147;
 Matches 503; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 764 aggcctgacacatttaaaagagatatacaaaaattgtgacacaaaaggaatactcca 823
 Db 70 acgagacacataaaagagatatacaaaaattgtgacacaaaaggaatactcca 129
 Qy 824 ttgaagctctgtgagacattccagagagagatgacacactactcogataitgacggc 883
 Db 130 ttgaagctctgtgagacattccagagagagatgacacactactcogataitgacggc 189
 Qy 884 gactgacctcttgaaaaacactgatatgatatgatatgacacactcctcaagacctc 943
 Db 190 gactgacctcttgaaaaacactgatatgatatgatatgacacactcctcaagacctc 249
 Qy 944 ttgaaagaaagctacacacttgactatgctatgttggttgagagaccttctcta 1003
 Db 250 ttgaaagaaagctacacacttgactatgctatgttggttgagagaccttctcta 309
 Qy 1004 ctccagtaggtcagttacagtagattcgtgtgacatgacatgacagaaagacaca 1063
 Db 310 ctccagtaggtcagttacagtagattcgtgtgacatgacatgacagaaagacaca 369
 Qy 1064 cacatagagatcgcacacacacacagacgacctcttgaatcaggtgttagctcaaca 1123
 Db 370 cacatagagatcgcacacacacacagacgacctcttgaatcaggtgttagctcaaca 429
 Qy 1124 atggaagctgtaattgtgatgacccagggagacacactcgaagcacaatcacagctc 1183
 Db 430 atggaagctgtaattgtgatgacccagggagacacactcgaagcacaatcacagctc 489
 Qy 1184 atgcaaggtgtaattgtgagagagaaagctaaagtctgttctttaaagaaagga 1243
 Db 490 atgcaaggtgtaattgtgagagagaaagctaaagtctgttctttaaagaaagga 549
 Qy 1244 agaagactgctcagcgcacacagtga 1269
 Db 550 agaagactgctcagcgcacacagtga 575

RESULT 12
 ID ABL19467 standard; DNA: 2153 BP.
 AC ABL19467;
 DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9874.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PE 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Claim 1; SEQ ID NO 9874; 21pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB57737-AB572072).
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 2153 BP; 679 A; 502 C; 475 G; 497 T; 0 other;
 SQ

Query Match 33 6%; Score 426.2; DB 23; Length 2153;
 Best Local Similarity 66.5%; Pred. No. 3.4e-123;
 Matches 611; Conservative 0; Mismatches 308; Indels 0; Gaps 0;
 QY 104 ctggggtctctatgtgtggaacccaacttcaggggttgcaagaagatagatgtggaact 163
 DB 579 ccggtgactatgtgtgcgcgaacatttcgtgtgtaaaaaatggtgtgtaattc 638
 QY 164 tcggagagccagcattatgtaaaaaatctcaacccaatgatatgtatgaacataactg 223
 DB 639 ttggcgaattgcgttgtaaaaaacattacacacattgacatgacatgacataaatg 698
 QY 224 aaccaataaatacagctgcgcacagcttcattatgagatgacatgatttaaacagctg 283
 DB 699 agcctatgaaatgaagctccgcgaactacacattagatgattgatttaaacattag 758
 QY 284 gcaagtgcaggtgaagttctccacaggtgtattactttgacacattggtggaataatag 343
 DB 759 gatcacatgagaggggtgacagaagtattacttcggccatgcggaataacatg 818
 QY 344 ccattgtgtcgtgagctccctcctcctagctgtgaggaactgtgtgacctgtgacgaa 403
 DB 819 ctctgttatagtgagttgtctgtgcacacttgaaagatttattcgatttgcgcagac 878
 QY 404 cattacttgaagacggtgttaattatagcactcagctgcttcctcgaatggaatag 463
 DB 879 gtccaacttgaagacggtgtctctctatgactatcacaattacccaacggaatcgaatg 938
 QY 464 tgcactaagaacccatttaccagatgtcaagcagaagaacttcctcattgttcgac 523
 DB 939 ttcatagtcgcacctaataatataagagtgatgaaacagaagaacttcctcattgtgcagaa 968
 QY 524 aaggaataaagaagcagatgtatacacattatgaacttggatggtgcgaagaataca 553
 DB 999 cgtcacaaaacgtgaaaaaattatataattattcgtgttggcgaagaataca 1058
 QY 584 ttgaccgcgaacacaaaacacatacctattatagggaacacaaagtcttaccggaactg 643
 DB 1059 ttgattatgataaataagcattacacatattcgtggaagcattacccaacggaacg 1118
 QY 644 caagatatatgtcatcaaacacgcatcttgcaagaagcaaacgcggaagattgtg 703
 DB 1119 caagttataatgatacaaacacgacatggtgtgagcagctgcgaacggaatgattgtg 1178
 QY 704 aagccctagcagcatgttcatgtatttccttcgaggaagcctccctcgtgcaagaactca 763
 DB 1179 aggcattgggcacataatgtatttatttcttaagggttccatcgcgtgcgaagcctaa 1238

QY 764 agcgtcacattaaaagagagatatcaaaaattgtgacccaacaaagatatccca 823
 DB 1239 agcgtgtacacccaagaagagatatcaaaaatcgggtgatacgaacgcaacgcca 1298
 QY 824 ttgaagctctctgtgaagaactttccagagagatgagcaacacttcgatattgcagc 883
 DB 1299 tcgagtgcttgtgtatgacacccggaagagattgtgacacatttcgltatgtacgc 1358
 QY 884 gactggaacttcttgaaaaacccgattatgattttacggaacctcttcacgaacctc 943
 DB 1359 ggtatgatttttcgaacacccgactatgatttcgcgaagactgtttcaagactat 1418
 QY 944 ttgaaaagaagctacacacttgcactatgcctatgtatggttggagacctatccca 1003
 DB 1419 tcgatgtgaaggatatacaccgagcagggcgagttcgcattgacaggaagaacatgtcaa 1478
 QY 1004 ctccagtaggttcagttca 1022
 DB 1479 cgcccgctgcgactctgtca 1497

RESULT 13
 AA217700
 ID AA217700 standard; cDNA; 447 BP.
 XX
 AC AA217700;
 XX
 DT 12-OCT-1999 (first entry);
 XX
 DE Human gene expression product cDNA sequence SEQ ID NO:5173.
 XX
 DE Human; gene; gene expression product; diagnosis; therapy; probe;
 KW detection; mapping; tissue typing; profiling; forensic; cancer;
 KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN M09938972-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 28-JAN-1999; 99WO-US01619.
 XX
 PR 03-APR-1998; 98US-0080666.
 PR 28-JAN-1998; 98US-0072910.
 PR 24-FEB-1998; 98US-0073554.
 PR 31-MAR-1998; 98US-0080114.
 PR 03-APR-1998; 98US-0080515.
 XX

PA (CHTR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Crivenjakov R, Dickson M, Drmanac R, Drmanac S;
 PI Escobedo J, Garcia AD, Garcia V, Giese K, Innis MA;
 PI Jones WR, Kassam A, Kennedy GC, Kita D, Labat I;
 PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
 PI Stache-Crain B, Sudduth-Klinger J, Williams LT;
 XX
 DR WPI; 1999-494092/41.
 XX
 PT Novel human genes and their expression products which are
 PT differentially expressed in different cell types
 XX
 PS Claim 1; Page 2451; 2479pp; English.
 XX
 CC The present invention describes a library of human polynucleotides
 CC comprising the sequences given in AA212532 to AA217779. Also described is
 CC a method of detecting differentially expressed genes correlated with the
 CC cancerous state of a mammalian cell, comprising detecting at least one
 CC differentially expressed gene product in a test sample from a cell
 CC suspected of being cancerous, where the gene product is encoded by one
 CC of the 5248 polynucleotide sequences given in AA212532 to AA217779. The

50 Sequence 447 BP; 129 A; 106 C; 106 G; 104 T; 2 other;

Matches 365; Conservative 1; Mismatches 7; Indels 4; Gaps 3;

QY 769 gacacattaaagagatatcaaaaattggtgacaccaaaggaatactccattgaa 828

Db 1 gacacatlaaagagatatcaaaaattggtgacaccaaaagyaatactccattgaa 60

QY 829 gccctctgtgagaactttccagagggagatggcaacctactctgatatgtcagggcactg 888

DB 61 gctcctctgtagaaccttccagagagatggaacaacctaccttcgatattgtcagggcactg 120

089 yacccccccgaaaccggagcgcacggagcccccacaggaccccccga 948

[illegible][illegible][illegible][illegible]

100

07 1126 ===== 1111

Db 361 aaaaactgaatat 377

AAC48459

10 ENCLOSURE, DNR, 140/ DF.
XX

[illegible][illegible]

XX

KW protein identification; signal transduction pathway;

XX
C
C
A
1
2
3
4
5
6
7
8
9
+
-
*
/

XX
PN
EP1033405-A2

XX 06-SEP-2000 .
PD

25-FEB-2000; 2000EP-0301439.

PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144684.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145092.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146389.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147204.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148365.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155386.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144684.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145092.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146389.
PR	02-AUG-1999;	99US-0146389.
PR	0	

```

Db 474 tctcaaacacacagcatattccatcacaggggaacaaacgaacctactctggaacagctcg 513
Qy 648 atatatgtctataacacagcatcttgcgaagaagccggagagatgatttggaaagc 707
Db 534 atatgaagtgttaaacacacacatcttgaaattgacgaagtagaaggatgatctggaac 593
Qy 708 cctgaagccatgatttcatcttctcttgcgaagcaccctccctgcgaagatcgaagc 767
Db 594 tctgaagctatcgtctatgatttcttctcgaagaaacctcttgcgaagcagccttcgtcg 653
Qy 768 tgaacatttaaaagagatatacaaaaatttgcacacaaaggaatactcccatga 827
Db 654 aggtaccacaaaagcagaataatgacacagatcagtgaaagaagaaagctaacacagtgga 713
Qy 828 agctctctgtggaacttccagaggagatggaacactcctcgatgatacgagcagact 887
Db 714 ggtccctgttaaaaacttccacactgagtcacatcgatttctctctatgctgcttcaat 773
Qy 888 ggaactctcttgaaaaacccgattatgagatattacggaacctcttcaagacctcttga 947
Db 774 acggtttgaagacaaacccagattatcaccctaaagagccttccagagaccttattat 833
Qy 948 aagaagagctacaccttgactatgcctatgattgag 984
Db 834 ccgagaaggttatcagttcagttgactatgattgattgag 870

```

RESULT 15
AA215033
ID AA215033 standard; cDNA: 300 BP.

AC AA215033;

DT 12-OCT-1999 (first entry)

DE Human gene expression product cDNA sequence SEQ ID NO:2502.

KW Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.

OS Homo sapiens.

PN W09938972-A2.

PD 05-AUG-1999.

PF 28-JAN-1999; 99WO-US01619.

PR 03-APR-1998; 98US-0080666.

PR 28-JAN-1998; 98US-0072910.

PR 24-FEB-1998; 98US-0075954.

PR 31-MAR-1998; 98US-0080114.

PR 03-APR-1998; 98US-0080515.

PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

PI Ervenjakov R, Dickson M, Drmanac R, Drmanac S;

PI Escobedo J, Garcia PD, Garcia V, Giese K, Inlis MA;

PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;

PI Lamson G, Lashkovitz D, Pot D, Randazzo F, Reinhard C;

PI Stache-Crain B, Sudduth-Klinger J, Williams LT;

DR WPI: 1999-749092/41.

Novel human genes and their expression products which are differentially expressed in different cell types

Claim 1; Page 1223; 2479pp; English.

The present invention describes a library of human polynucleotides comprising the sequences given in AA21532 to AA21779. Also described is

a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA21532 to AA21779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.

Sequence 300 BP; 94 A; 67 C; 62 G; 77 T; 0 other;

Query Match 23.6%; Score 300; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.9e-84;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 769 gacacattaagaagagatatacaaaaattggtgacacaaagaataccctctga 828
Db 1 gacacattaagaagagatatacaaaaattggtgacacaaagaataccctctga 60
Qy 829 gctctctgtggaacttccagaggagatggaacactcctcgatgatacgagcagactg 888
Db 61 gctctctgtggaacttccagaggagatggaacactcctcgatgatacgagcagactg 120
Qy 889 gactctcttgaaaaacccgattatgagatattacggaacctcttcaagacctcttga 948
Db 121 gactctcttgaaaaacccgattatgagatattacggaacctcttcaagacctcttga 180
Qy 949 aagaagctacaccttgactatgcatgattggttggagagacctctactca 1008
Db 181 aagaagctacaccttgactatgcatgattggttggagagacctctactca 240
Qy 1009 gtaggtcagtcacgtagattctgtgcatctgcaataactcgagaagaccacacat 1068
Db 241 gtaggtcagtcacgtagattctgtgcatctgcaataactcgagaagaccacacat 300

```

Search completed: August 17, 2002, 22:19:54
Job time: 6863 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:23:16 ; Search time 50.12 Seconds
(without alignments)
6219.252 Million cell updates/sec

Title: US-09-765-068-1
1269
Sequence: 1 atgaccatctagtaagga.....ctgcacgcgcacaagtga 1269

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/CTOS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Dackfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608.8	48.0	2405	1	US-08-454-097-30 Sequence 30, Appl
2	608.8	48.0	2405	3	US-08-185-359-30 Sequence 30, Appl
3	564.8	44.5	1233	1	US-08-454-097-32 Sequence 32, Appl
4	564.8	44.5	1233	3	US-08-185-359-32 Sequence 32, Appl
5	279.6	22.0	3505	1	US-08-454-097-34 Sequence 34, Appl
6	279.6	22.0	3505	1	US-08-468-036-43 Sequence 43, Appl
7	279.6	22.0	3505	2	US-08-376-843-43 Sequence 43, Appl
8	279.6	22.0	3505	2	US-08-185-359-34 Sequence 34, Appl
9	267.8	21.1	1210	1	US-08-447-500-7 Sequence 7, Appl
10	267.8	21.1	1210	1	US-08-454-097-7 Sequence 7, Appl
11	267.8	21.1	1210	1	US-08-453-866-7 Sequence 7, Appl
12	267.8	21.1	1210	3	US-08-185-359-7 Sequence 7, Appl
13	267.8	21.1	1779	1	US-08-447-500-9 Sequence 9, Appl
14	267.8	21.1	1779	1	US-08-453-866-9 Sequence 9, Appl
15	267.8	21.1	2914	3	US-08-454-097-11 Sequence 11, Appl
16	267.8	21.1	2914	3	US-08-185-359-11 Sequence 11, Appl
17	262.2	20.7	2468	1	US-08-468-036-19 Sequence 19, Appl
18	262.2	20.7	2468	2	US-08-376-843-19 Sequence 19, Appl
19	262.2	20.7	2469	1	US-08-447-500-3 Sequence 3, Appl
20	262.2	20.7	2469	1	US-08-454-097-3 Sequence 3, Appl
21	262.2	20.7	2469	3	US-08-453-866-3 Sequence 3, Appl
22	262.2	20.7	2469	3	US-08-185-359-3 Sequence 3, Appl
23	237.4	18.5	1520	3	US-09-100-664A-1 Sequence 1, Appl
24	234.2	18.5	1485	1	US-08-468-036-8 Sequence 8, Appl
25	234.2	18.5	1485	2	US-08-376-843-8 Sequence 8, Appl
26	234.2	18.5	3098	1	US-08-447-500-1 Sequence 1, Appl
27	234.2	18.5	3098	1	US-08-454-097-1 Sequence 1, Appl

28	234.2	18.5	3098	1	US-08-447-408-1 Sequence 1, Appl
29	234.2	18.5	3098	1	US-08-453-866-1 Sequence 1, Appl
30	234.2	18.5	3098	3	US-08-185-359-1 Sequence 1, Appl
31	225.2	17.7	1989	1	US-08-447-500-5 Sequence 5, Appl
32	225.2	17.7	1989	1	US-08-454-097-5 Sequence 5, Appl
33	225.2	17.7	1989	1	US-08-453-866-5 Sequence 5, Appl
34	225.2	17.7	1989	3	US-08-185-359-5 Sequence 5, Appl
35	195.4	15.4	1689	1	US-08-447-500-11 Sequence 11, Appl
36	195.4	15.4	1689	1	US-08-453-866-11 Sequence 11, Appl
37	195.4	15.4	2385	1	US-08-454-097-9 Sequence 9, Appl
38	195.4	15.4	2385	1	US-08-468-036-41 Sequence 41, Appl
39	195.4	15.4	2385	2	US-08-376-843-41 Sequence 41, Appl
40	195.4	15.4	2385	3	US-08-185-359-9 Sequence 9, Appl
41	162.8	12.8	3627	1	US-08-447-500-23 Sequence 23, Appl
42	162.8	12.8	3627	1	US-08-454-097-23 Sequence 23, Appl
43	162.8	12.8	3627	1	US-08-453-866-23 Sequence 23, Appl
44	162.8	12.8	3627	3	US-08-185-359-23 Sequence 23, Appl
45	162.8	12.8	3628	1	US-08-468-036-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-454-097-30
Sequence 30, Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..1197

QY	1	atggaccatcctctatgttggggaagaagtgtaagaacaacggaacacccaacccaatggcgaaca	60
Db	25	ATGGAAAATATAAAAAGAAAGCAAGACGAATCATGATGATGAAATGGCAGCACTATGTTGGT	84
QY	61	aggagtcacaacgycctctgcacacatctgtctctcaatctctctcgtcgtgggtctctatgtg	120
Db	85	CGATCGGACACACACACTCGAGCACTGGGTCTTCATCG--TCTGGAGTTTAAATGGTT	141
QY	121	ggaccacccttcagggtttggccaagaagataagatgtggaaccttcggaagctcagaata	180
Db	142	GGACCTAACTTTAGAGTGGAAAAAAATTTGGATGTCGCAATTTTGGAAATTACGATTA	201
QY	181	ggtaaaaactctacacccaatgatatagtcagcaatcaactgaaaccaataataatcagct	240
Db	202	GGGAAAAATTTAAACCAATGAAATGTGGCAATTAATTGAGCCCATGAAATCAAGA	261
QY	241	gtctcaagcttaatttagtgatcacatattttaaagccttggaagctggagcggggaaggt	300
Db	262	GCACACAGCTACATTTGGATTAACAATTCCTTAAGCAATTG---GATCTGGAGATGGT	318
QY	301	ctcccaacagctgatcactcttgacacatgttgggaaataataatgcatgtgtcgtgagctc	360
Db	319	ATACCTCAATTTACATTTTCGGCCCCCTGTGGTAAATACAAAGCATATGGTGTGGAATG	378
QY	361	cttggccctatgcttggagaagcttgtttgaacctgtlgacgcgaacatctaacttgaagcg	420
Db	379	CTGGGACCTGTGTTGGAAAGCTTTGTGACTGTGTGACAGAACATTTTCTCTTAAACA	438
QY	421	gtgttaattgtaacatccacgctgtcttcttgatbgaatatagttgactccaagaagctc	480
Db	439	GTTCCTCATGATCTATPACACTGATTTCTCGATGGAATATGCTCATTCAAAGAACTTG	498
QY	481	attaccagagctgtcaagccagaagaactccctgatttgcgcgaacgaataagaagaag	540
Db	499	ATTATACGAGATGTGAAAACCTGGAACCTTTAATATGACGACAGCAAGAAACCAACCG	558
QY	541	catgtatacacatbatagaacttggaccttgcgcgaagaatatacatgaccccgaaaccaa	600
Db	559	CAATTTATTCACATTTATATGATTTTGGTTTGGCAAGAAAGAAATATATGATCCGAGCAAG	618
QY	601	aaaacactacctatagggaacccaagaagttaactcgsaacctgcgaagatataatgtctac	660
Db	619	AAACACATACCATPACAGAGAACACAAAGACCTTTACGAGAACGCTPAGATATATGACATA	678
QY	661	aacagcagcttgcgaagaagcgaagccgagagatgatttgaagccctagccatagc	720
Db	679	AACACACATTTAGGAAAAGACAAATATAGAGAGACGATTTGAAGCTTTAGGTATATG	738
QY	721	tctcatgattctcttcgaggaagcagccctctgcgcaagatcctaagcctgcagacatlaaa	780
Db	739	TTTATGTATTTTTCGAGAGCACTTCCTCTGGCAAGCCTTAAAGCTGACACATTAAG	798
QY	781	gagagatatcaaaaatgtgtgacacccaagaagaatactcccatgtgaagctctctgtgag	840
Db	799	GAGAGCATATGAAAAATTGGAGATACAAAACGGCTACACCAATGTGAAGTGTATAGTAA	858
QY	841	aacttcagaagagataggaagaacctccttcgatatagtcagaacgcctgcgactctctgaa	900
Db	859	AATTTTCCAGAGAAATGGCAACATATCTTCGTATGTATGAAAGGCTTGATTTTGTAA	918
QY	901	aaacctgattatgattattacaggaccccttcacagacaccccttctgaaaagaagaagctac	960
Db	919	AAACCAACATATGACATCTTAAGAAAAGCTTTTACAGATGTTTGTGACGAAAAGATAT	978
QY	961	accttgcatactgcatagtatggtgttggagaacctatctcactccagtaggttcagtt	1020
Db	979	ATGTTTATATATGATATGTGACTGATTTGGTAAACAACTTCCCTACCTCCAGTGGGTGCACTT	1038
QY	1021	caagtaattctgtgcatctgtgcaataaactcgaaagaagcacaacataggaatgagca	1080
Db	1039	CAGCAATCTCTGCTGTATTAACA---GAGAAACACATCAACACGAGATTAAGTG	1095

Oy	1081	tcnaacagcagcctcttgaatctggtgtagtatcaaccaatggagagctgaagtc	1140
Db	1096	CAACATCCAA-----AAACGAGTTGTAGTTCTACAAATGGAGAGTTAAACCA	1146
Oy	1141	gatatcccaaggagagcccatccaatgcacatcaagccatcgccaggtgaggtta	1200
Db	1147	GATACCCCAACGAG-ACGTTCTAAATGACCCCATACAGCCCTTACTAGTAGAAGT	1205
Oy	1201	gtgaggaagctaagtgcgtgcttcctttaagag	1236
Db	1206	ATGGATGAACCAACTCCAGAAAGTGTGAACATG	1241

```

1      RESULT      3
2      US-08-454-097-32
3      ; Sequence 32, Application US/08454097
4      ; Patent No. 5686412
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Hoekstra, Merl F.
8      ; TITLE OF INVENTION: Protein Kinases
9      ; NUMBER OF SEQUENCES: 57
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
12     ; STREET: 233 South Wacker Drive, 6500 Sears Tower
13     ; CITY: Chicago
14     ; STATE: Illinois
15     ; COUNTRY: USA
16     ; ZIP: 60606-6402
17     ;
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: Patent In Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/454,097
25     ; FILING DATE: 30-MAY-1995
26     ; CLASSIFICATION: 424
27     ;
28     ; PRIOR APPLICATION DATA:
29     ; APPLICATION NUMBER: 08/185,359
30     ; FILING DATE: 21-JAN-1994
31     ; APPLICATION NUMBER: US 08/008,001
32     ; FILING DATE: 21-JAN-1993
33     ; PRIOR APPLICATION DATA:
34     ; APPLICATION NUMBER: US 07/728,783
35     ; FILING DATE: 03-JUL-1991
36     ;
37     ; ATTORNEY/AGENT INFORMATION:
38     ; NAME: No. 5686412and, Greta E.
39     ; REGISTRATION NUMBER: 35,302
40     ; REFERENCE/DOCKET NUMBER: 27866/31853
41     ; TELECOMMUNICATION INFORMATION:
42     ; TELEPHONE: 312-474-6500
43     ; TELEFAX: 312-474-0448
44     ;
45     ; TELEX: 25-3856
46     ; INFORMATION FOR SEQ ID NO: 32:
47     ; SEQUENCE CHARACTERISTICS:
48     ; LENGTH: 1233 base pairs
49     ; TYPE: nucleic acid
50     ; STRANDEDNESS: single
51     ; TOPOLOGY: linear
52     ; MOLECULE TYPE: cDNA
53     ; FEATURE:
54     ; NAME/KEY: CDS
55     ; LOCATION: 1..1041
56     ;
57     ; US-08-454-097-32

```

	Query Match	Similarity	Score	DB 1:	Length
	Best Local	72.7%	Pred. 2.6e-173		
	Matches	803: Conservative	0: Mismatches	282: Indels	19: Gaps
Qy	133	agggttgcgaagaagatagatctggaacttcggaagctcagattagtaaaatctc	192		
Db	1	AGAGTTGGCAAAAAAATTGGATGTCGCATTGGAGTAATTCGATTAGCGAAAAATTTA	60		


```

Db 566 -----TGGGGAAGAGGCAACCTGGTGTACATCACTTCGGGGTGGCCAAAGCT 619
QY 581 acatigaccgcgaacaaacacacataccttataggaacacaaagttaactggaa 640
Db 620 ACCGGGATGACGACGACCAACCAACATCCCTATGTGTAGAAAGAAACCTCACGGGA 679
QY 641 ctgcaagatatatgtctatcaacacgcatcttggcaagaacgcggaagatgatt 700
Db 680 CCGCGGGGTACCCCTCCATCAACACGCACTTGAATTGAACATCCCAAGAGATGACT 739
QY 701 tggagacccttaggcacatagttcacatatttcttccttgaggacgccccttcggaagac 760
Db 740 TGGAGCTCTGGGCTACGTGCTAAATGTACTTCAACTGGGGCTCTCCCTGGCAGGGCT 799
QY 761 tcaagctgacacattaaagagagatatacaaaaaattgtgtacacacaaagaataacc 820
Db 800 TGAAGGCTGCCACCAAGACAGAAATACGAAGATTTCGCAAGAAATGTCCACCC 859
QY 821 ccattgaagctctctgtgagaaacttccagagagagatggcaacctacattcgatgtca 880
Db 860 CCATGGAAGTGTGTGAAGGCTTACCCCTCCGAATTGGCCACATACCTGAATTTCTGCC 919
QY 881 ggcgactgacctctcttgaanaaactgtattatagattatattaggaacctctcacagacc 940
Db 920 GTTCCTTGCGTTTACGACGACAGCCTGACTACTCGTACCTGGCAGCTTTCCGGAAATC 979
QY 941 tcttgaanaaagaaagctacacatttgactatgctatgatttgg 984
Db 980 TGTTCATCGCCAGGCGTTCTCTATGACTAGTGTGACATGG 1023

RESULT 6
US-08-468-036-43
: Sequence 43, Application US/08468036
: Patent No. 5728806
: GENERAL INFORMATION:
: APPLICANT: Demaggio, Anthony J.
: APPLICANT: Hoeksma, Merl F.
: TITLE OF INVENTION: Materials and Methods Relating to Proteins that
: INTERACT WITH CASEIN KINASE I
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468, 036
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,605
: FILING DATE: 21-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: NO. 5728806and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/31784
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 43:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3505 base pairs
: TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-468-036-43

Query Match      22.0%; Score 279.6; DB 1; Length 3505;
Best Local Similarity 58.9%; Pred. No. 1.9e-80;
Matches 521; Conservative 0; Mismatches 354; Indels 9; Gaps 2;

QY 101 cctctgggttcttatgtgtgggacccaacttaaggttggcaagaagatagatgtgga 160
Db 149 CCGCATGGAGCTGAGAGTGGGAAACAGGTACCGGCTGGCGGAGAAATGCGACCGCT 208
QY 161 acttcggaagctcagataggtaaaatctctacacccatgaatcagatagatcaaac 220
Db 209 CCTTGGAGACATCTATCTCGGTAGGACATTCGCGAGAAAGATGTCATCAAC 268
QY 221 tggaaacataaatacagtgctccagcttcaattagatagacagatttaaacagc 280
Db 269 TTGAATGTGTCAAAACCAACACCCCTCAGCTCCACATGAGAGCAAAATCTACA 325
QY 281 ttggcagtgaggtgaaaggtctcccaaggtgattactttggaccatgtggaatata 340
Db 326 TGATCCAGGAGAGAGTGGGCAATCCACCATGATGATGGGGGCGGAGAGGGGACTACA 385
QY 341 atgcacatgtgtgagctccttggcccttagcttggaggaactgttgaacctgtgacc 400
Db 366 ACGTATGTGATGAGAGCTGCTGGGGCCAGCGCTGGAGAGCTCTTCAACTTCTCTCCA 445
QY 401 gaacattacttgaagaagtgtaataagatccacacagctgtcttcgaatggaat 460
Db 446 GGAATTCAGCCTCAAAACCCGCTGCTGTGTGACCAATGATGATGATGATGATGAT 505
QY 461 acgtgactcaagaacactcattaccagatgtgtaacccagagaaacttctgtatgtc 520
Db 506 ACATTCAATCAAAAGACTCATCCACCGGGAGTGAACCCAGACCAACTTCTCAAGGGCC 565
QY 521 gacaagcaataaagaagaagcatgttataacattatagacttggatggccaaagaaat 580
Db 566 -----TGGGGAAGAGGGAACCAACGCTGTGATCATGACTGCGGTGGCCAAAGAGT 619
QY 581 acatigaccgcgaacaaacacacataccttataggaacacaaagttaactggaa 640
Db 620 ACCGGGATGACGACGACCAACCAACATCCCTATGTGTAGAAAGAAACCTCACGGGA 679
QY 641 ctgcaagatatatgtctatcaacacgcatcttggcaagaacgcggaagatgatt 700
Db 680 CCGCGGGGTACCCCTCCATCAACACGCACTTGAATTGAACATCCCAAGAGATGACT 739
QY 701 tggagacccttaggcacatagttcaatgtatttctctcggagcagcctccctcggaagac 760
Db 740 TGGAGTCTCTGGGCTACGTGCTAAATGTACTTCAACTGGGGCTCTCCCTGGCAGGGCT 799
QY 761 tcaagctgacacattaaagagagatatacaaaaattgtgtgacacaaagaataacc 820
Db 800 TGAAGGCTGCCACCAAGACAGAAATACGAAGATTGAGGAAGAAATGTCCACCC 859
QY 821 ccattgaagctctctgtgagaaacttccagagagagatggcaacctacattcgatgtca 880
Db 860 CCATGGAAGTGTGTGAAGGCTTACCCCTCCGAATTGGCCACATACCTGAATTTCTGCC 919
QY 881 ggcgactgacctctcttgaanaaactgtattatagatttcaaggaacctcttcacagacc 940
Db 920 GTTCCTTGCGTTTACGACGACAGCCTGACTACTCGTACCTGGCAGGCTTTCCGGAAATC 979
QY 941 tcttgaanaaagaaagctacacatttgactatgctatgatttgg 984
Db 980 TGTTCATCGCCAGGCGTTCTCTATGACTAGTGTGACATGG 1023

RESULT 7
US-08-376-843-43

```


DB 371 CTTAAGGTGGGTT---GGCATCCCCACATFACGGTGTGTGTCAGGAAAAAGACTAC 427
QY 340 aatgcattgctgagagctccttgccctagcttgaggaacttgcttgacctgtgac 399
DB 428 AATGTACTAGCATGATCTTCTTGAGACTGACCTCGAACCTCTTCAATTTCTGTCA 487
QY 400 cgaacattacttgaagagctgtaataatgataagcaccagctgtcttcgcgaatgaa 459
DB 488 AGAAGGTTCAACATGAATAACTGTAATGTTAGTCTGACCGAGATGATGAGTAATGAA 547
QY 460 taactgacataaagaacacttattaccgagatgtaagcagaagaacttctgattgt 519
DB 548 TATGTGATACAAAGAAATTTTATACAGACATTAACAGATTAACCTCTTAATGGGT 607
QY 520 cgaacagcaataaagaagacatgattatatacatattagacttgactgccaagaa 579
DB 608 ATTGGGCTCAGCTGTAATAG-----TTATCTTATTTGATTTTGGTTGGCCAAAAG 661
QY 580 tacattgaccccgaaacaaacacatactattagaggaaacaaagttaactgga 639
DB 662 TACAGAGACAACAGACAGGCAACATACATACAGAGAAGATAAAACCTCAGTGGC 721
QY 640 actgcaagatatagtctatacaacagcatcttgcaagaagcaagccgagagatgat 699
DB 722 ACTGCCGATATGCTTACATCAATGACATCTTGTATGTAGCGAGACTGCCGAGATGAC 781
QY 700 ttggaagcccaagacataatgtaatttcttccctgaggaagcccccctgcaagaa 759
DB 782 ATGGAATCATATGATATGTTTATGATTTTATGAAACACGCCCTGCGCAAGAGG 841
QY 760 ctcaagagctgcacataaagaagagataatcaaaaaatggtgacacaaagaactact 819
DB 842 CTAAAGCTGCACAAAGAAACAAATAATGAAAGATAGTAAAGATGTCCACG 901
QY 820 cccattgaagctctctgtagaacttcccaagagagatgagcaacttctgtagatgc 879
DB 902 CCTTTAAGTTTATGATTAAGGGGTTCTCGAAGTTTGGAATTTAACTAATTTGT 961
QY 880 aggaagctgagactctcttgaaacccgattatgattatgaagccctcttcacagac 939
DB 962 CGTGGGCTACCTTTGAAGAAAGCCCGCATTAATGATGATGAGGAGCAGCTATTCG 1021
QY 940 ctcttgaagaagaagctacacacttgactgactgactgactgactgactgactg 984
DB 1022 CTTTACAGACCTGAAACATCATATGACTACACATTTGATGG 1066

RESULT 10
US-08-454-097-7
Sequence 7, Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merf F.
TITLE OF INVENTION: Protein kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Protein Kinase
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1147
US-08-454-097-7

Query Match 21.18; Score 267.8; DB 1; Length 1210;
Best Local Similarity 58.18; Pred. No. 6.6e-77;
Matches 514; Conservative 0; Mismatches 362; Indels 9; Gaps 2;

QY 100 tccctcgtgggtcttctatgctgagagcccaactcaggttgagcaagaatagatgag 159
DB 191 TCCAGGCTGAATTCATTTGCGAGGAAATATACTGTCAGCAAGATGGGCTCTGCG 250
QY 160 aactcggagagctcagatagtgtaaaatctctacacaaatgaatatgtagaatcaa 219
DB 251 TCCATTGGGAGCATCTATTGCGGATCAACATCACCAAGCGGAGAGTGGCGTGAAG 310
QY 220 ctggaaccaataaataatcagtgctcccaagcttattatgagtgatgagtgatgag 279
DB 311 CTGAATCTCAGAGGCGAGGACATCCCAAGTGTGTGACGAGACAGCTCTATAAGATT 370
QY 280 ctgagcagtgcaagtggaagctctcccaagtgatattacttgagcaatgaggaatat 339
DB 371 CTTCAAGGTGGGTT---GGCATCCCCACATACGGTGTGTGTCAGGAAAAAGACTAC 427
QY 340 aatgcattgctgagagctccttgccctagcttgaggaacttgcttgacctgtgac 399
DB 428 AATGTACTAGCATGATCTTCTTGAGACTGACCTCGAACCTCTTCAATTTCTGTCA 487
QY 400 cgaacattacttgaagagctgtaataatgataagcaccagctgtcttcgcgaatgaa 459
DB 488 AGAAGGTTCAACATGAATAACTGTAATGTTAGTCTGACCGAGATGATGAGTAATGAA 547
QY 460 taactgacataaagaacacttattaccgagatgtaagcagaagaacttctgattgt 519
DB 548 TATGTGATACAAAGAAATTTTATACAGACATTAACAGATTAACCTCTTAATGGGT 607
QY 520 cgaacagcaataaagaagacatgattatatacatattagacttgactgccaagaa 579
DB 608 ATTGGGCTCAGCTGTAATAG-----TTATCTTATTTGATTTTGGTTGGCCAAAAG 661
QY 580 tacattgaccccgaaacaaacacatactattagaggaaacaaagttaactgga 639
DB 662 TACAGAGACAACAGACAGGCAACATACATACAGAGAAGATAAAACCTCAGTGGC 721
QY 640 actgcaagatatagtctatacaacagcatcttgcaagaagcaagccgagagatgat 699
DB 722 ACTGCCGATATGCTTACATCAATGACATCTTGTATGTAGCGAGACTGCCGAGATGAC 781

Oy	700	tttaaaagcccaaggccatatagtcatatcttcctcgagagcaagcccccctgcgaaga	75
Db	782	ATGAGATCATTTAGCATATGTTTATATATTTTATATGAACCGAGCTGCATGCGAAGG	841
Oy	760	ctcaagagctgacacattaagaagagatalcaaaaaatctggtacaccgaagaataact	819
Db	842	CTAAGGCTGCACAAAGAAACAAAATATGAAAAGTTGTGTAAAAAGAAAGATGTCCAG	901
Oy	820	cccaattgaagctctctgtggaacttcctcagagagagatgagcaaccctatgatgac	879
Db	902	CCTGTGTAAAGTTTATATGTAAGGGGTTTCCCTGCGAATTTCCGATGTAATCTTAATTTGT	961
Oy	880	aggcgactggaactctcttgaaaaaactgatalatagataltacggaacccctcttcaagac	939
Db	962	CGTGGGCTACGCTTTGGAGGAGGCCCCAGATTAATCATGTATCGAGCAGCATATCCGATT	1022
Oy	940	ctctcttgaagaagaagctacacacttgatcatatgcatgcatatgttg	984
Db	1022	CTTTTCAGAGCCCTGAAACCATCATATATGATCTACATCATATTGATTTGG	1066

RESULT 11

```

US-08-453-866-7
: Sequence 7, Application US/08453866
: Patent No. 5756289
:
: GENERAL INFORMATION:
: APPLICANT: Hoechst, Merl F.
: TITLE OF INVENTION: PROTEIN KINASES
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Judas & Lubitz
: STREET: 1880 Century Park East, Suite 500
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90067
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/453,866
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/008,001
: FILING DATE: 20-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Wetherell Ph.D., John R.
: REGISTRATION NUMBER: 31,678
: REFERENCE/DOCKET NUMBER: PD-2458
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ. ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1210 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: IMMEDIATE SOURCE:
: CLONE: Protein Kinase
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 173..1147
:
: US-08-453-866-7

```

Query Match	21.1%;	Score 267.8;	DB 1;	Length 1210;
Best Local Similarity	58.1%;	Pred. No. 6.8e-77;		

Matches	514; Conservative	0; Mismatches	362; Indels	9; Gaps
QY 100	tcctctggtgttcttaatgctggtggaacccaacttaaggcttgagcaagaagatgattggg	159		
Db 191	TCCAAGGCTCAATTCATTTGCTGGGGGAAATATAAATCGTGTACGGAAGATCGGGTCTGGC	250		
QY 160	aacttgagagagcctcagattagtgtaaaaactcttaacccaatgaatatagtatgaatcaaa	219		
Db 251	TCCTCTCGGGACATCTATTGTGGGATCATACATACCAACGAGGCAAGAACTGGCAGTGAAG	310		
QY 220	ctgagacaataaatcaatcacgtgtctccacagctcattatagatagacagattataacag	279		
Db 311	CTGAAATCTGAGAAAGGCGCAGCATCCCACTTCTGTACGAGAGCAAGCTCTATAAGATT	370		
QY 280	cttgagcagctgagctgtaaggctccacagtgattactttgagcaatgtyggaatat	339		
Db 371	CTTCAAGGTGGGGT---GGCATCCCGACATACGGTGGATGTGTCAGAGAAAAGACTTAC	427		
QY 340	aatgcatgtgtcttgtagagctccctctggccctagcttgtaggaactgtgttaacctctgtac	399		
Db 428	AAATGTAATCTATGATGGATCTTCTGGGACCTGAGCCTGGAAGACCTCTCAATTTCTGTCCA	487		
QY 400	cgaacattctcttgtagaagcgtgttaataatgataagcatcacagctgtttcttgaatgga	459		
Db 488	AGAAAGTTTCAATGAAATCTGACTTATGTTATGCTGACCAATGATCATGTAATTTGAA	547		
QY 460	taagtgcactcaagaagactcatttaacgagatgltcaaaagccagaagaaactcttgattgt	519		
Db 548	TATGTGATCTCAAAAGATTTTATACACAGAGACATTTAAACAGATTAATCTTAATGGGT	607		
QY 520	cgaagaagcacaataagaagaagcatgtataacattatataagactttgagctgagcaagaa	579		
Db 608	ATTGGGCGTCACTGATATAAG-----TTATTCCTTATGATTTTGGTTGGCCAAAAG	661		
QY 580	tacattgaccccgcaaaccaaaaacacataccttaattaggaacacaaagtttaactga	639		
Db 662	TAAAGAGACAAACAGGCAAGGCAACATACCTTACAGAGAAAGATTAATAAATCTCACTGGC	721		
QY 640	actgcagaatatagtctataccaacagcatcttgccaagaagcaaaagccggagagatgat	699		
Db 722	ACTGCCCGGATCTCTAGCATCATATGACACATCTTGGTATGTGACAAAGTGGCCGAGATGAC	781		
QY 700	ttagaagcccttaggcataatgttcaatgatttccctctggagagactccctcggaagaa	759		
Db 782	ATGGAATCATTTAGGATATGTTTTGATGATTTTAAATAGAACCAAGCCTCCAGAGGCAAGG	841		
QY 760	ctcaagcgtgcacacatlaaagagagatatcaaaaatattgtygcacccaagaagaaact	819		
Db 842	CTTAAAGCTGCAACAAGAAACAAAATATGTAAAGATTAGTGAAGAAAGATGTCTCACG	901		
QY 820	cccatggaagctctctgttagaacttccacagaagagatgacacacttacccttcgatatgc	879		
Db 902	CCGTGTGAAGTTTATGTAAAGGGGTTTCTGTGAGATTTGCCATGTACTTAAACATATGT	961		
QY 880	aggcgacatgacttctttgaaaaaacctgtatagagattacaggaacctcttcacagac	939		
Db 962	CGGGGCTCTACGTTTGTAGGAAGCCCGCAGATTCATGTATCTGAGGCACTTATTCGCAATT	1021		
QY 940	ctctttgaaaagaagagctacacacttgtagctgtgctatgattgg	984		
Db 1022	CTTTTAGAGACCTGAACCATATATGTGCTCAACATTTGATTTGG	1066		

RESULT 12

US-08-185-359-7
: Sequence 7, Application US/08185359
: Patent No. 6060296
: GENERAL INFORMATION:
: APPLICANT: Hoekstra, Merl F.
: TITLE OF INVENTION: Protein Kinases
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

DB 518 AATTAAGTATGATGATCTTCTTGAGACCTAGCTCGAAGACCTTCAATTTGTGTCA 577
QY 400 cgaacattacttgaagacggttataatagacacacagctgtcttcgaatgaa 459
DB 578 AGAAGTTCAACATGAAGTACTTATGTAGTACGACGATGATGATGATGAA 637
QY 460 taagtgaactaaagaacatttaccagatgtcaagcagaacattccatgtgt 519
DB 638 TATGTGATACAAAGATTTTATACAGAGACATTAACGATTAACCTTCATATGGGT 697
QY 520 cgaacaggaataaagaagacatgttatcacatitacatttgaagcagaagaa 579
DB 698 ATTGGGGCTACTGTAATTAAG-----TTATCTTTTATGATTTGGTTGGCCAAAAG 751
QY 580 tacattgaccccgaaacaaacacacatacattatagggagacaaagttaactgga 639
DB 752 TACAGAGACAACAGACGACACATACATACAGAGATTAACCTCAGTGGC 811
QY 640 actgcaagatatatgtctatcaacacgcatcttgcaagaagacggagagatgat 699
DB 812 ACTGCCGATATGCTACATCAATGACATCTTGATATGAGCAGAGTCGCCGAGATGAC 871
QY 700 ttggaagccctgaagcatalgtatgtatcttcccttgagagcagctcccttgcaagaa 759
DB 872 ATGGAATCATATTAGATATGTTTATGATATTAATGAAACCACTGCTGACGAGGG 931
QY 760 ctcaaggtctgaacattaaagaagatalcaaaaaatgttgacacacaaagaataact 819
DB 932 CTAAAGGCTGACAAAGAAACAAATTAAGAAAGATTAAGAAAGATGATGACG 991
QY 820 ccaattgaagctctgttggaacattccagagagagatggaacattccctgatatgtc 879
DB 992 CCTGTGAAGTTATGATTAAGGGGTTCTGCAAGATTTGCGATGATCTTAACATATTGT 1051
QY 880 agggagctgacattcttgtaaaaaacattatgagatattcaagaccccttcacagac 939
DB 1052 CGTGGCTACCTTTTGAGGAGGCCCGACATTAATCATGATCTGAGGACGATTTCCGATT 1111
QY 940 cctcttgaagaagaagctacacatttgacatgtcctatgatgtg 984
DB 1112 CTTTTCAGAACCTCGAACCATATGACTACATCACTTGTGTTGG 1156

RESULT 15
US-08-454-097-11
; Sequence 11, Application US/08454097
; Patent No. 5686412
; GENERAL INFORMATION:
; APPLICANT: Hoechst, Merl F.
; TITLE OF INVENTION: Protein Kinases
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,097
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185,359
; FILING DATE: 21-JAN-1994
; APPLICATION NUMBER: US 08/008,001
; FILING DATE: 21-JAN-1993

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,783
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5686412and, Grete E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3836
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2914 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 265..1275
; US-08-454-097-11

Query Match 21.1%; Score 267.8; DB 1; Length 2914;
Best Local Similarity 58.1%; Pred. No. 1.2e-76;
Matches 514; Conservative 0; Mismatches 362; Indels 9; Gaps 2;

QY 100 tcccttggtgtcttactatgtgtgagcccaactcaggggttgcaagaagatagatgtgg 159
DB 283 TCCAGAGCTGATATCATTTGTCGGAGGGAATTAACGATGAGGAGATGGGTCTGCG 342
QY 160 aactcggagagctcagatagtagtaaaatctcaaccaatgatatgtagcaatcaa 219
DB 343 TCCCTCGGGGCATCTATTGGCGATCAATCAACCAACGCGAGAGTGGCGTGAAG 402
QY 220 ctggaaccaataaataacagtgctcacaagctcattatagagatagatattataaag 279
DB 403 CTGAATCTCAGAAAGCCAGGACATCCCGATTGCTGTAAGAGACCAAGCTTATTAAGTT 462
QY 280 ctgagcagtcgaagtggaaggtctcccaaggtgtatcttacttggacatgtggaatlat 339
DB 463 CTTCAAGTGGGGT---GGCATCCCAACATAGGATGATGATGATGATGATGATGATGAT 519
QY 340 aatgcatagtgtcgtgagctccttgccctagcttggagagattgttaccctgtgac 399
DB 520 AATTAAGTATGATGATCTTCTGAGACCTGACCTCGAAGACCTTCAATTTCTGTCA 579
QY 400 cgaacattacttgaagacggttataatgaacacacacagctgtcttcgaatgaa 459
DB 580 AGAAGTTCAACATGAAGTACTTATGATCTGACCGAGATGATGATGATGATGATGATGAT 639
QY 460 taagtgaactaaagaacatttaccagatgtcaagcagaacattccatgtgt 519
DB 640 TATGTGATACAAAGATTTTATACAGAGACATTAACCAAGATTAACCTTCATATGGGT 699
QY 520 cgaacaggaataaagaagacatgttatcacatitacatttgaagcagaagaa 579
DB 700 ATTGGGGCTACTGTAATTAAG-----TTATCTTTTATGATTTGGTTGGCCAAAAG 753
QY 580 tacattgaccccgaaacaaacacacatacattatagggagacaaagttaactgga 639
DB 754 TACAGAGACAACAGACGACACATACATACAGAGATTAACCTCAGTGGC 813
QY 640 actgcaagatatatgtctatcaacacgcatcttgcaagaagacggagagatgat 699
DB 814 ACTGCCGATATGCTACATCAATGACATCTTGATATGAGCAGAGTCGCCGAGATGAC 873
QY 700 ttggaagccctgaagcatalgtatgtatcttcccttgagagcagctcccttgcaagaa 759
DB 874 ATGGAATCATATTAGATATGTTTATGATTAATTAAGAACCAAGCTGCGATGCGAGGG 933
QY 760 ctcaaggtctgaacataaagaagagatatacaaaaatgtgtgacacacaaagaataact 819

```
Db 934 CTAAGGCTGCACACAAAGAAATATGAAAGATTAGTGAAGAAGATGTCCACG 993
Oy 820 cccattgaagctctctgtgagaaacttccagagagatggcaaccttcgatatgic 879
Db 994 CCTGTTGAAGTATTATGTAAGGGGTTTCCTCGCAGAAATTGGCATGTACTTAACATAATTGT 1053
Oy 880 aggcgactggaacttcttgaaaaaacctgattatgagatttlaaggaacctcttcacagac 939
Db 1054 CGTGGGCTACGCTTTGAGGAAGCCCGAGATTACATGTATCTGAGGAGCTATTCCGCAAT 1113
Oy 940 ctcttgaagaagaagctacacaccttgactatgacctatgattgg 984
Db 1114 CTTTCAGGACCCCTGAACCATCAATATGACTACACATTGATTGG 1158
```

Search completed: August 17, 2002, 21:27:32
Job time: 3856 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:18:06 ; Search time 1693.47 Seconds
(without alignments)
10113.929 Million cell updates/sec

Title: US-09-765-068-1

Perfect score: 1269
Sequence: 1 atgagcaccctccagtagga.....ctgcacagcgcacaaagta 1269

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

ESR:*
1: em_estda:*
2: em_esthm:*
3: em_estln:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615.4	48.5	930	10	BF308810 601869729
2	599	47.2	935	9	AL524795
3	560	44.1	940	9	AL526554
4	495.8	39.1	841	10	BE786814
5	494	38.9	885	10	BI196952
6	480.8	37.9	594	10	BI390112
7	471.8	37.2	847	10	BI409005
8	464.8	36.6	889	10	BM008018
9	461.4	36.4	776	10	BM007847
10	435.4	34.3	466	10	W90174
11	434.2	34.2	759	9	AJ394482
12	432	34.0	868	10	BG745206
13	416.8	32.8	777	10	BM049421
14	414.2	32.6	553	9	AV614943
15	413.4	32.6	466	9	AA210141
16	413	32.5	844	10	BM048132
17	403.4	31.8	836	10	BI664914

18	400.8	31.6	659	9	AL633314	AL633314
19	386.2	30.4	828	10	BE562448	BE562448 601335911
20	380.8	30.0	688	10	BI739265	BI739265 603359555
21	379.4	29.9	727	10	BG260877	BG260877 603372475
22	379.4	29.9	962	10	BF980670	BF980670 602304390
23	375.4	29.6	826	10	BM048049	BM048049 603620375
24	368.8	29.1	861	10	BG398668	BG398668 602440275
25	367.2	28.9	613	10	BE793767	BE793767 601589918
26	366.6	28.9	819	10	BI104367	BI104367 602889951
27	366.4	28.9	906	10	BF160061	BF160061 601167749
28	364.6	28.7	656	9	AW990004	AW990004 u133a04.y
29	364.2	28.7	885	10	BG387674	BG387674 602412530
30	361.8	28.5	637	10	BF141805	BF141805 601787674
31	354	27.9	716	10	BG249775	BG249775 602319428
32	352.8	27.8	527	9	AW652323	AW652323 100239 MA
33	350.6	27.6	691	9	AW127769	AW127769 f197g11.y
34	347.4	27.4	706	10	BE374102	BE374102 601228144
35	347	27.3	715	10	BE732523	BE732523 601565540
36	346.8	27.3	821	10	BI085586	BI085586 602870125
37	346.2	27.3	648	10	BG335875	BG335875 602404596
38	344.2	27.1	373	9	AA210142	AA210142 mu42902.r
39	344.2	27.1	812	10	BG740368	BG740368 602634131
40	343.4	27.1	838	10	BI911256	BI911256 603063069
41	341.2	26.9	845	9	AL558268	AL558268 AL558268
42	339.8	26.9	1041	10	BF237650	BF237650 601841826
43	339.6	26.8	575	10	BG085938	BG085938 H3119H06-
44	339.4	26.7	878	10	BE900116	BE900116 601673020
45	336.6	26.5	842	9	AI892993	AI892993 mq91h03.y

ALIGNMENTS

RESULT 1
BF308810 930 bp mRNA linear EST 21-NOV-2000
DEFINITION 601869729F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:413494 5',
LOCUS mRNA sequence.
ACCESSION BF308810 GI:11256075
VERSION BF308810.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 930)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LNCM1008 row: 1 column: 07
High quality sequence stop: 684.
location/Qualifiers
1. 930
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4123494"
/clone_id="NIH_MGC_17"
/issue_type="ribodm/sarcoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: muscle; vector: pORF7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(c). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University

FEATURES

source

of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 BASE COUNT 261 a 223 c 236 g 210 t
 ORIGIN

Query Match 48.5%; Score 615.4; DB 10; Length 930;
 Best Local Similarity 97.9%; Pred. No. 4.3e-159;
 Matches 698; Conservative 0; Mismatches 6; Indels 9; Gaps 7;

```

Oy 72 ctgcccacacatctgtgctctctatcgccctgggtcttattgttggagcccaatt 131
    |||||||
Db 2 ctgctctgcacacatctgctctctctatcgccctgggtcttattgttggagcccaatt 61
Oy 132 cagggtctggcaagaatagatgattgtgggaactctggagagctcagattagtaaaatct 191
    |||||||
Db 62 cagggtctggcaagaatagatgattgtgggaactctggagagctcagattagtaaaatct 121
Oy 132 ctacacccaatgataatgtatgcaatacaactggaaaccaataataacgtgtctccacagct 251
    |||||||
Db 122 ctacacccaatgataatgtatgcaatacaactggaaaccaataataacgtgtctccacagct 181
Oy 252 tcaattagaatcacatattatacaacagcttgagagctgaggtgaggtctcccaagct 311
    |||||||
Db 182 tcaattagaatcacatattatacaacagcttgagagctgaggtgaggtctcccaagct 241
Oy 312 gtattactctggacacatctgggaataatataatgcaatgtgtctgagctctctggccctag 371
    |||||||
Db 242 gtattactctggacacatctgggaataatataatgcaatgtgtctgagctctctggccctag 301
Oy 372 ctgtgaggaactgtgttgacacctgtgtgacccgaacatttacttggagaggggtttatgat 431
    |||||||
Db 302 ctgtgaggaactgtgttgacacctgtgtgacccgaacatttacttggagaggggtttatgat 361
Oy 432 agccatccaagctgtctctcgatgataatgacgtgacatccaagaacctcattaccgaga 491
    |||||||
Db 362 agccatccaagctgtctctcgatgataatgacgtgacatccaagaacctcattaccgaga 421
Oy 492 tgtcaagccagaagaactctctgattgtgtcgaagaagcaataaagaagcaltgtatata 551
    |||||||
Db 422 tgtcaagccagaagaactctctgattgtgtcgaagaagcaataaagaagcaltgtatata 481
Oy 552 catatagaactctgtgacgtggccgaagaataatcttgaaccccgaaacaaaacacatacc 611
    |||||||
Db 482 catatagaactctgtgacgtggccgaagaataatcttgaaccccgaaacaaaacacatacc 539
Oy 612 ttatagggaacacaaagttaactggaactgcaagatatgtctatcaacagcatct 671
    |||||||
Db 540 ttatagggaacacaaagttaactggaactgcaagatatgtctatcaacagcatct 598
Oy 672 tggcaaaagagcaaaagccggaagagatgttggaaagccctaggccatatgttcatatt 731
    |||||||
Db 599 tggcaaaagagcaaaagccggaagagatgttggaaagccctaggccatatgttcatatt 656
Oy 732 ccttgagagagagcctccctctgagagagctcaaggtcagacataataaagaaga 784
    |||||||
Db 657 ccttgagagagagcctccctctgagagagctcaaggtcagacataataaagaaga 705

```

RESULT 2

AL524795 935 bp mRNA linear EST 13-FEB-2001
 LOCUS AL524795 LTI.NFL003.NBC3 Homo sapiens cDNA clone CS0DC008Y123 5
 DEFINITION AL524795 LTI.NFL003.NBC3 Homo sapiens cDNA clone CS0DC008Y123 5
 prime, mRNA sequence.
 ACCESSION AL524795
 VERSION AL524795.1 GI:12788288
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 935)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 location/Qualifiers

Source

1. 935

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DC008Y123"

/clone_id="LTI.NFL003.NBC3"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with NotI and

cloned into the NotI and EcoRV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed

by life technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610

8371 Email : fliang@life.com URL :

http://fulllength.invitrogen.com"

BASE COUNT

247 a 235 c 231 g 220 t

2 others

ORIGIN

Query Match

47.2%; Score 599; DB 9; Length 935;

Best Local Similarity

100.0%; Pred. No. 1.5e-154; Length 935;

Matches 599; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 671 ttggcaaaagagcaaaagccggaagagatgtatttggaaagccctaggccatatgttcatgtatt 730
    |||||||
Db 1 ttggcaaaagagcaaaagccggaagagatgtatttggaaagccctaggccatatgttcatgtatt 60
Oy 731 tccctcgagagcagctccctctgcaagagactaaaggtcgacacattaaagaagagatattc 790
    |||||||
Db 61 tccctcgagagcagctccctctgcaagagactaaaggtcgacacattaaagaagagatattc 120
Oy 791 aaaaaattgtgtacacaaagaagaatactcccatgtgaagctctctgttgaagactcttcag 850
    |||||||
Db 61 tccctcgagagcagctccctctgcaagagactaaaggtcgacacattaaagaagagatattc 120
Oy 121 aaaaaattgtgtacacaaagaagaatactcccatgtgaagctctctgttgaagactcttcag 180
    |||||||
Db 121 aaaaaattgtgtacacaaagaagaatactcccatgtgaagctctctgttgaagactcttcag 180
Oy 851 aggaagatgcaaaccttactctgataatgcaagagcagctggaactcttcttgaagaaactgatt 910
    |||||||
Db 181 aggaagatgcaaaccttactctgataatgcaagagcagctggaactcttcttgaagaaactgatt 240
Oy 911 atgagatattacgagacccctctcagagacactcttggaaagaagaagcttcaacactttgact 970
    |||||||
Db 241 atgagatattacgagacccctctcagagacactcttggaaagaagaagcttcaacactttgact 300
Oy 241 atgagatattacgagacccctctcagagacactcttggaaagaagaagcttcaacactttgact 300
    |||||||
Db 241 atgagatattacgagacccctctcagagacactcttggaaagaagaagcttcaacactttgact 300
Oy 971 atgctatgattgggttggagagactattcttactccagataggtcagttcagttacgtatt 1030
    |||||||
Db 301 atgctatgattgggttggagagactattcttactccagataggtcagttcagttacgtatt 360
Oy 301 atgctatgattgggttggagagactattcttactccagataggtcagttcagttacgtatt 360
    |||||||
Db 301 atgctatgattgggttggagagactattcttactccagataggtcagttcagttacgtatt 360
Oy 1031 ctgtgtcatctgtcaataactcgagaagccacacacataaggaatgcgcacatcaacagc 1090
    |||||||
Db 361 ctgtgtcatctgtcaataactcgagaagccacacacataaggaatgcgcacatcaacagc 420
Oy 1091 agcctctcgaaatacagtggtttagctcaacaaatggagagctgaaattgtttagtctcca 1150
    |||||||
Db 421 agcctctcgaaatacagtggtttagctcaacaaatggagagctgaaattgtttagtctcca 480
Oy 1151 cggagagccacatcccaatcaacacacagctcagtcgaggttggaggttagtggaggaag 1210
    |||||||
Db 481 cggagagccacatcccaatcaacacacagctcagtcgaggttggaggttagtggaggaag 540
Oy 1211 ctaagtgtcgtgttcttctaagaggaagaagaagactgtctcagcgcacaagatga 1269
    |||||||
Db 541 ctaagtgtcgtgttcttctaagaggaagaagaagactgtctcagcgcacaagatga 599

```

```

RESULT      3
AL226554    AL226554      940 bp      mRNA      linear      EST 13-FEB-2001
LOCUS       AL226554 LrL_NFL003_NBC3 Homo sapiens cDNA clone CS0DC014F07 5
DEFINITION  prime, mRNA sequence.
ACCESSION   AL226554
VERSION     AL226554.1  GI:12790047
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 940)
AUTHORS     Li,M.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 940
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC014F07"
/clone_1ib="LrL_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT      244 a      248 c      222 g      226 t

Query Match      44.1%; Score 560; DB 9; Length 940;
Best Local Similarity 100.0%; Pred. NO. 9.1e-144;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 taagccatatgtcatgtatttcttcctcgagagagcctccctggcaagactcaaggctg 769
|||||
DB 1 TAGGCATATGTTCAATGATTTCTTCGAGGAGCCTCCCTCGCAAGACTCAAGGCTG 60
|||||
QY 770 accattaaagagagatatacaaaaattgtgacaccaaagaagatattccattgaag 829
|||||
DB 61 ACACATTAAAGAGATATCAAAAATTGCTACACCAAAAGAAATACCTCCATTGAAG 120
|||||
QY 830 ctctctgtgaaacttccagagagatgagcaacttactctgatalgtcagcgactg 889
|||||
DB 121 CTCCTGTGTGAACTTCCAGAGAGATGCAACCTACCTGATATGTCAGGCGACTG 180
|||||
QY 890 actctctgaaaaaactgtatatttcaagaccccttccacagaccttttgaag 949
|||||
DB 181 ACTTCTTTGAAAAACCGATTATGAGATTATGAGACCCCTTCAAGACCTTTGAAA 240
|||||
QY 950 agaaagctacaccttgaactatgacctatggtgttgagagactattccactccag 1009
|||||
DB 241 AGAAAGCTACACCTTGTGACTATGCTATGATGGGTGGGAGACCTATTCTACTCCAG 300
|||||
QY 1010 taaggttcagttcagttcagttcgtgtcattcgtcaataactcgagaagcacacata 1069
|||||
DB 301 TAGGGTCAGTTCAGTAGATTCTGTGCAATCTGCATAACTCGAAGAACACACATA 360
|||||
QY 1070 ggagtcggccatcaacaagcagcctcttcgaatacagtggttaagctcaaccaatgag 1129
|||||

```

```

DB 361 GGCATCGCCATCACACACAGCAGCTCTTGAATACAGTGTTAGTCAACCAATGAG 420
|||||
QY 1130 agctgaattgttatgatccacgagagaccactccaatcacaatcagctcagcg 1189
|||||
DB 421 AGCTGATGTTGATGATGCCAGGAGCCACATCCATATGACCAATACAGCTCATCGC 480
|||||
QY 1190 aggttgaggttagttgaggaagcctaagtgcctgcttcttctaagaggaaggaaga 1249
|||||
DB 481 AGCTGAGGCTAGTGGAGGAAGCTAAGTGTCTGTTCTTAAAGAGAAAAGAAAGA 540
|||||
QY 1250 ctgctcagcgccacaaagtga 1269
|||||
DB 541 CTCGTCAGCCGACCAACTGA 560
|||||

RESULT      4
BE786814    BE786814      841 bp      mRNA      linear      EST 20-OCT-2000
LOCUS       BE786814 601477624F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880565 5',
DEFINITION  mRNA sequence.
ACCESSION   BE786814
VERSION     BE786814.1  GI:10208012
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 841)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9647 row: p column: 06
High quality sequence stop: 551.
Location/Qualifiers
1. 841
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3880565"
/clone_1ib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by life
Technologies."

BASE COUNT      257 a      210 c      212 g      162 t

Query Match      39.1%; Score 495.8; DB 10; Length 841;
Best Local Similarity 94.7%; Pred. NO. 5e-126;
Matches 567; Conservative 0; Mismatches 27; Indels 5; Gaps 5;

QY 667 catcttgcaaaagcaaaagcggagagatggaagcctcagagcatatgttcattg 726
|||||
DB 1 CATCTAGGCAAAAGCAAAACCGAGAGATGATTAGAAACCCCTAGGCCATATGTTACT 60
|||||
QY 727 taattccttcgagcgagcctccctggcaagagcctcaaggctcagacattaaagagaga 786
|||||
DB 61 GTATTTCCTTCAAGGAGCTCCCTCGCAAGACTCAAGGCTGACACATTAAAGAGAGA 120
|||||
QY 787 tatcaaaaattgtgtacaccaaagaagatattccatttaagctctctgtggaactt 846
|||||

```


Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	121	TATCAAAA-TGCTGACACCCAAAAGAAATACTCCCATTTGAAGCTCTCTGTGACACTTT	885 bp	EST 10-JUL-2001				
Qy	847	ccagagagatgycgaacctacccttcgatalgtcaggcgac--tgsactctcttgaaaaaac	885 bp	EST 10-JUL-2001				
Db	180	CCAGAGGAGATGGCAACTACTCTTGATATGTGACAGGCACATGACACTCTTTGAAAAAAC	885 bp	EST 10-JUL-2001				
Qy	906	tgatattagatattacggaccctctctacagacctcttgaagaagaagcttaacct	885 bp	EST 10-JUL-2001				
Db	240	TGATTATAGATATTTACGACCCTCTTTCACAGACTCTTTGAAAAAGAAAGCTACACTT	885 bp	EST 10-JUL-2001				
Qy	966	tgaactatgcctatgatttggtgtggagagacctatctcctacccagtaggttcagttacgt	885 bp	EST 10-JUL-2001				
Db	300	TGACTATGCTATGA-TGGTGTGGGAGACCTATACCTACTCCAGTAGAGGTACGTACAGT	885 bp	EST 10-JUL-2001				
Qy	1026	agattctgtgtcattctgcaataactccgagaaagccacacacataggatcgtccatca	885 bp	EST 10-JUL-2001				
Db	359	AGATTCTGTGTGATGTGCAATTAACTCGAGAAAGCCACACACTATAGGATGGCCATCCCA	885 bp	EST 10-JUL-2001				
Qy	1086	acagagacctctctgaaatacagtggtgttagctcaaccacatggagagcgtgaatgtcatga	885 bp	EST 10-JUL-2001				
Db	419	ACAGACGCTCTTTCGAAATCAAGTGTGTAGCTCAACACAAATGAGAGCTGAATGTGATGA	885 bp	EST 10-JUL-2001				
Qy	1146	tcccaacggagcccaatcccaatgcaacaaatcacagctcatgcccgggtggagtagtga	885 bp	EST 10-JUL-2001				
Db	479	TCCACGGGAGAGCCACTCCCAATGCACCAATCACATGCATGCGCAGAGGTGGAGGTGTGGA	885 bp	EST 10-JUL-2001				
Qy	1206	ggaagctaatgac-tgcgtttctcttaagagaga--aaagaaagaagactgctagcgca	885 bp	EST 10-JUL-2001				
Db	539	GGAACCTAAGTCTCTGCTGTACTTAAAGAGAACAGAGAACGACACTGCTCAGCGCA	885 bp	EST 10-JUL-2001				
RESULT	5	BI196952	885 bp	EST 10-JUL-2001				
LOCUS	BI196952	602755974P1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4891363 5',						
DEFINITION	BI196952	mRNA sequence.						
ACCESSION	BI196952	BI196952						
VERSION	BI196952.1	GI:14651961						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
TITLE	NIH-MGC http://mgc.nci.nih.gov/.							
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)							
COMMENT	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: cgsbpb-jemail.nih.gov							
	Tissue Procurement: ATCC							
	cDNA Library Preparation: Ling Hong/Rubin Laboratory							
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)							
	DNA Sequencing by: Incyte Genomics, Inc.							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov							
	Plate: LCM1770 row: d column: 20							
	High quality sequence stop: 879.							
FEATURES	Location/Qualifiers							
SOURCE	1..885							

BASE COUNT	194 a	280 c	265 g	146 t
Query Match	38.9%, Score 494; DB 10; Length 885;			
Best Local Similarity	74.6%; Pred. No. 1,66-125;			
Matches 661; Conservative	0; Mismatches 220; Indels 5; Gaps 3;			
DB	1	GGTGGGCCCCCACTTCCCGCTCGGCMAAAGATCGGCTCGCGCAACTTCGGGGAGACTCCG	60	
QY	117	ggtggaccaccaactcagggtgtgcaagaagatagatgtgtggaaacttcgaagactcaag	176	
DB	1	GGTGGGCCCCCACTTCCCGCTCGGCMAAAGATCGGCTCGCGCAACTTCGGGGAGACTCCG	60	
QY	177	attagtgtaaaatctctcaccaagaatgatgtgtgcaataacactggacccaataaaatc	236	
DB	61	CCTAGGAAAGAAATCTCTATACAAATGAATACCTGGCTATCAATTTGGAGCCGATCAAGTC	120	
QY	237	acgtctccacagcttcatttagagtaacagatttatataaagcttgcagtgcaagtga	296	
DB	121	CGGGGCCCCCGACAGCTGCACCTGGAATACCGGTCTCAAGAGAGCT---CAAGCCACAGCA	177	
QY	297	aggtccccaacagtgatattacttggacccabtgtyggaataataatgcatgtgtgtga	356	
DB	178	GGGGGCTCCCTCAGGCTACTACTCTGTCGTCGGCCGGGAGAAATCAACGCCATGTGCTCGA	237	
QY	357	gtctcttggccctagacttggagagacttgttgactctgtgacccgaacatttactttgaa	416	
DB	238	GCTGCTGGGGGCCACCCCTGGAGGAGACTTCTGCACCTGGCACCGGACTTCACGCTCAA	297	
QY	417	gaaggtgttaatgataagacatccagctgtctctctcgaaatggatacgtgcactcaagaa	476	
DB	238	GACGGTGTGATGATCGGCATCCACTATACCGCGCATGAGATGTGTCACACCAAGAG	357	
QY	477	ccctacttaccgagatgtgcaagccagagaaactctctgtatgtgcgcaaggcaatcaagaa	536	
DB	358	CCTATATACCGGAGGAGTGAAGCCCGAAGAACTCTGTGTGGGGCCCGCGGAGACCAACG	417	
QY	537	agagacatttatacaacattatagaaacttggagacttgcaggaataacatttgcgccgaac	596	
DB	418	GCAGCATCCCATCCATCATCATCATGACTTGGGGTGGCCAAAGAGATACATCGACCCCGAAGC	477	
QY	597	caaaaacacatcacatttaaggaaacacaaaagtttaactgtgaactgcagaatatatc	656	
DB	478	CANAGAGACATATCCCGTACCGGACACAAAGAGCTGACGGGACAGGGCCCTACATGAG	537	
QY	657	tatcaacacgcactcttggcaaaagccggaagagatgaaatttggaaagcccttagcca	716	
DB	538	CATCAACACGCACTGGGCAAGAGCAAGAGCGCGCGCACACGACGCGAGCGGCTGGGCCA	597	
QY	717	tatgtcatgtatctccctctggagagagctccctctggaaagagatccaaggtgtgcaactt	776	
DB	598	CATGTTCATGTATCTTCCTCGCGCGGAGCGCTCCCTCGGAGGGGCTCAAGAGCGCGACGCT	657	
QY	777	aaaagaagagatacctaaaatgtgtgcacccaagaagaaatactcccatgtgaactctgtg	836	
DB	658	CANAGAGCGGATACGAAAGATGGGGACACCAAGCGCCACAGCCCATCGAGTCTGTG	717	
QY	837	tgaagacttcccaaggagatgcaacacta--ccttgcataatgtcagcgcaactgtctct	895	
DB	718	CGAGAACTTCCAGAGGAGATGGCCACAGACCCCTGATGTGGCGGCTGACTCTCT	777	
QY	896	ttgaaaacactgatatagtaatttaaggaccctcttcaag--acacttctgaaaagaa	954	
DB	778	TTTCGAGAGCCGACATGATGACTCTCCCTCGCGAAGCTTTACCGAATCTTTTCGACCGAGT	837	
QY	955	ggctacacacttgactatgacctatgtattgtgtgtgagaaactatcc	1000	
DB	838	GGCTTCGTGCTGACTATGAGTAGACACTGGGCGGGAGGCCCTTGC	883	

Library Gallus gallus cDNA clone pGp1c-pK03.d8.5' similar to
 g111545751 ref|NP_071331.1| casein kinase 1, gamma 1 [Homo sapiens
] dbj|BAB17838.1| (AB042562) casein kinase 1 gamma 1 [Homo sapiens
], mRNA sequence.
 BI390112
 accession BI390112.1 GI:15083394
 version EST
 keywords EST
 organism Gallus gallus
 source chicken
 ORIGIN
 chicken.
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 594)
 REFERENCE
 1 Porter, T.E. and Cogburn, L.A.
 ESTs from Primary Chicken Pituitary/Hypothalamus/Pineal cDNA
 library USDA/IRAFs Animal Genome Project
 Unpublished (2001)
 JOURNAL
 Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburnudel.edu, www.chickest.udel.edu.
 FEATURES
 source
 location/Qualifiers
 1..594
 /organism="Gallus gallus"
 /strain="Commercial broiler chicken"
 /db_xref="taxon:9031"
 /clone="pGp1c-pK03.d8"
 /clone_lib="Primary Chicken Pituitary/Hypothalamus/Pineal
 library"
 /sex="Male and Female"
 /tissue="Pituitary Gland/Hypothalamus/Pineal Gland"
 /dev_stage="Embryonic (dl2,dl4,dl9); post-hatch (w1,w3,w5
 ,w7,w9)"
 /lab_host="E. coli EM8DH108"
 /note="Vector: pCMVSPORT6. Library made from equivalent
 pools of total RNA isolated from each tissue at different
 ages. Single pass sequencing from 5'-end"
 BASE COUNT 185 a 145 c 128 g 131 t
 ORIGIN
 Query Match 37.9%; Score 480.8; DB 10; Length 594;
 Best Local Similarity 87.9%; Pred. No. 6e-122;
 Matches 521; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Db 362 GTCATTCACATCATAGACTTTGGAGCTGGCAGAGAGTACATTTGACCCAGAACCCAAAA 421
 QY 604 cacatcctataggagacacaaagtcttacttggaactcgaatatatgctataac 663
 Db 422 CACATACCTTACAGGAGAACACAAAGCTTAACGTGAAGCGGAGATACATGTCATAC 481
 QY 664 accgacttggcgaagcgaagcggagatgatattgggaagccgagcagatgttc 723
 Db 482 ACCGATCTTGCCAGAACGCAAAAGTCGAGATACCTTGGAGCCCTTGGCCACATGTT 541
 QY 724 atgatttcctcgaggcagctccctggcgaagactcgaagctgacacatt 776
 Db 542 ATGATTTCTCGAGACAGATCTGCCCTGGCAAGAGCTGANNNTGACACCTT 594
 RESULT 7
 BI409005 847 bp mRNA linear EST 14-AUG-2001
 LOCUS 602966091F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5121407 5',
 DEFINITION mRNA sequence.
 ACCESSION BI409005
 VERSION BI409005.1 GI:15169928
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 847)
 REFERENCE
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapds.rem@nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLM11296 row: e column: 24
 High quality sequence start: 7
 High quality sequence stop: 846.
 Location/Qualifiers
 1..847
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:5121407"
 /clone_lib="NCI_CGAP_Lu33"
 /tissue="pooled lung tumors"
 /lab_host="Dh10B (phage-resistant)"
 /note="Organ: lung; Vector: pTZ19D-pac (Pharmacia) with a
 modified polylinker. Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was prepared from mRNA obtained from pooled
 lung tumors with a NotI - oligo(dT) primer [5'
 TGTACCACTGTAAGTGGAGCGGCGCTGTGTTTGTGTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with NotI and cloned into the Not
 I and Eco RI sites of the modified pTZ19D vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 198 a 241 c 248 g 160 t
 ORIGIN
 Query Match 37.2%; Score 471.8; DB 10; Length 847;
 Best Local Similarity 74.9%; Pred. No. 2.2e-119;
 Matches 631; Conservative 0; Mismatches 207; Indels 5; Gaps 3;
 QY 143 agaaagtagatgtggaacttggagagctcagattaggtaaatctacacaaat 202

Db	9	AGAAATATGGCGTGTGGGAACTTCGCGGAGACTTCGCGCTAGGAAAGAAATCTGTATACAAATG	68
OY	203	ataatgtgccaatccaacttggaaaccaataaataacacgtgtccacagcttcattttagt	262
Db	69	AGTAGTGCGCTATTCAGAGCTGGAGCCCATCACTCCCGGGCCCCACAGCTGCACCTGGAGT	128
OY	263	acaagattataaagacttggcagtgacggtgaaaggtgtcccaagaggtatattacttg	322
Db	129	ACCGCTTTTACAGACGCTCAGACAGACA---GAGGGCTCCCTCAGGCTCTACTACTTG	185
OY	323	gaccaatgtgggaaatataatgcaatgtgtgtcgtgagctccttggccctagcttggagact	382
Db	186	GCCCTTTGTGGGAAGTACAAAGCCATGATGCTGGAGAGCTGCTGGGGGCCCACTGGAGAGACC	245
OY	383	tgtttgacctctgtgacccgaacatttactttaaagaggtgttaatagatgcattccacg	442
Db	246	TTTTTGACCTGTGGCACCGCACCTTCACGCTTAAGACGGTGTGATGATGGCCATCCAC	305
OY	443	tgcttcccgatagtgaatacgtgtcacctcaaaagacctcaatttaccgagatgtccaagcacg	502
Db	306	TGATACCGCGATGATGATGACGTGACACACCAAGAGCCTCATACCGTGAAGTGAAGCCCG	365
OY	503	agaacttccctgattgtgtgcagaagacataaagaagacatgtttataccattatagact	562
Db	366	AGAACTTCTCGTTGTGGGGCGCGGACAGAAACGGACAGCACTCCATCCATCATCTAGACT	425
OY	563	cttgcactggccaagaatacatattgacccccggaacaaacaaacacatactattaggaac	622
Db	426	TTGGGCTGGCCACAGAGATGATCGACCTCTGACACTTAAGAAGCATCCATTCGCGAGC	485
OY	623	acaaaagtttaacttgaactgcagaatgatatatgtctatacacacgaactcttggcaaaagc	682
Db	486	ACAAGAGCGCTGACAGAGCACTGCGGCTCATGACATCAACACGCACTTGGGCAAAAGAGC	545
OY	683	aaagccggaagatgatttggaaagccctgaagcattgtatgtatattccttggagga	742
Db	546	AGAGCGCGCGGATACCTCGAGGCGTGGGACACATGTTCAATGTACTCTCGCGGGGA	605
OY	743	gctccccccttggcaagactcaaggtctgaac-attaaagaagagatatataaaaatttgt	801
Db	606	GTCGCGCTGCGAGGGGCTCAAGGACAGACACGCTGAACGAGCGCTACAGAAAGATTGA	665
OY	802	gaacccaanaagaaataactcccatitgaagctctctgtgagaacttcccgagaagatggga	861
Db	666	GACACCAAGCGCTGCCACACCAATTCAGAGTGTGTGAAGCTTTCCCGGAGAGATGGCC	725
OY	862	accacacttgatatgttaagcgactgtgactcttcttgaaaaacccgattatgattta	921
Db	726	ACCTATTGGCGCTAAGTGTGCGGCGCTAAGACTTTTGTGAGAACCCAGACACTACACTACCG	785
OY	922	cgaagcctcttcaacagacctcttggaaaagaaaggtacacaccttgaactatgactatgt	981
Db	786	AGGAGAGCTCTACAGACACTCTTTT-ACCAGACGGGCTACGTTGTGACTACAAAGATATGAC	844
OY	982	tgg 984	
Db	845	TGG 847	

RESULT	8
LOCUS	BM008018
DEFINITION	889 bp mRNA linear EST 30-OCT-2001
ACCESSION	60361776.F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5451062 5',
VERSION	BM008018
KEYWORDS	BM008018.1 GI:16522372
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 889)
	NIH-MGC http://mgc.nci.nih.gov/ .

FEATURES	SOURCE
1. 889	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_image="5451062"
	/clone_id="NIH_MGC_113"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: spleen; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGAG(g). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
	High quality sequence stop: 857.
	Location/Qualifiers
	row: m column: 15
	Plate: LICM1940
	found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940
	row: m column: 15
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Email: cga@b-remail.nih.gov
	Tissue Procurement: Dr. Mark Watson
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LICM1940

Db 580 GCGGAGGAGGAGGCGGCTACATGACATCAACGACGACCTGGGCAAGAGGAGGACC 639
 Qy 689 ggagagatgatttgaagccctagagcatatgtcatgtatttcttcgagagccctcc 748
 Db 640 GCCCGAGGAGGAGGCGGCTGCGGCGACATGATCTTCTGCGGCGGAGCCCTCC 699
 Qy 749 cctggcaagagctgaagctgacacattaaagagagatcaaaaattgtgacacca 808
 Db 700 CCGGCAAGGAGGAGGCGGCTGCGGCGACATGATCTTCTGCGGCGGAGCCCTCC 759
 Qy 809 aagaataatcccatgaaagctctctgtgagaaatttcagagagatgagcaatcacc 868
 Db 760 AACCGGAGGAGGCGGCTGCGGCGACATGATCTTCTGCGGCGGAGCCCTCC 817
 Qy 869 ttgcatatgtaagcagcagctcttcttgaagaaacctgattatgatttaccagacc 928
 Db 818 TGCGCTATGTCGCGGCTGCGGCGACATGATCTTCTGCGGCGGAGCCCTCC 877
 Qy 929 tcttcacagacc 940
 Db 878 TCTTAACCGACC 889

RESULT 9
 BM007847 776 bp mRNA linear EST 30-OCT-2001
 LOCUS 60361753F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450743 5',
 DEFINITION mRNA sequence.
 ACCESSION BM007847
 VERSION BM007847.1 GI:16522201
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 776)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plate: LCM1939 row: p column: 08
 High quality sequence stop: 772.
 Location/Qualifiers
 1. 776
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5450743"
 /clone_id="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site: 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAGG(C). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC library."
 BASE COUNT 176 a 246 c 232 g 122 t
 ORIGIN
 Query Match 36.4%; Score 461.4; DB 10; Length 776;
 Best Local Similarity 75.6%; Pred. No. 1.6e-116;
 Matches 586; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

Qy 143 agaagataagatgtggaagcttcgagagcctcaagatagtaaaatcttaccacaa 202
 Db 2 AGAAGATCGGCTGGGCGCAACTTCGGGAGGCTCCGGCTAGAAAAGATCTGATACAAATG 61
 Qy 203 aatatgtagcaatcaaatggaacccaataaaatcaagtgctccacagcttcaattagat 262
 Db 62 AATACGTGGCTATCAAAATTTGAGCCGATCAAGTCCCGGGCCCCCGACCTGGACCTGGAGT 121
 Qy 263 acagatttataaacagcttgagcagtgagtgagtgagtgctcccaagtgatattacttg 322
 Db 122 ACCGGTCTTACAAACAGT---CAAGCGCACAGAGGCGCTCCCTAGGCTTACTACTTCG 178
 Qy 323 gaccatgtggaataatataatgctgctgagcagctccttggccctgagcttggagagct 382
 Db 179 GTCCGTGGGGAAGTACAAACGCAATGCTGCTGAGACTCTGGGCGCCAGCCTGGAGGAGC 238
 Qy 383 ttttgaaccttgtagccggaacatttacttgaagaagtggttaatgataacacagc 442
 Db 239 TGTTCGACCTGTGCGGAGCTTCAAGCTTCAAGACGCTGCTGATGATCGCATCCAGC 298
 Qy 443 tgccttcgaaatgaaatgacgtgacatcaagaagcatttaccagatgcaagcag 502
 Db 299 TGATCAGCGGATGAGATGTGCAACCAAGAGCTTATCTACCGGAGCTGAAGCCCG 358
 Qy 503 agaactcctgattgctgcaagcaataaagaagcagatgattatcacattatagact 562
 Db 359 AGAAGCTTCTGCTGGGCGGCGGCGGCGGACCAAGCGGACAGTCCATCATCATGACT 418
 Qy 563 ttgacttggccaagaaatatactgaccccgaaacccaacacacatattataggaac 622
 Db 419 TGCGGCTGCCAAGAGATGATATGCAACCCGAGACCAAGACATCCCGTACCCGAGC 478
 Qy 623 acaaaagttaactcggaaactcgaagatataatgctatcaacagcatttggcaagagc 682
 Db 479 ACAAGAGGCTGACGCGGCGGCGGCTGATGATGATGATGATGATGATGATGATGATGAT 538
 Qy 683 aagaacgagagagatgatttgaagccctgaagcatttgaatgatttcttcgagagc 742
 Db 539 AGAGCGCGGCGGAGGAGCTGGAAGGCGCTGGGCGACATTTCTATCTTCTCGCGCGCA 598
 Qy 743 gctccctctgcaagagctcaagagctgacacattaaagaagagatataaaatgtg 802
 Db 599 GCTTCCCTGGCAGAGGCTTCAAGGCGGACACGCTCAAGAGGCGTACCAAGATCGGGG 658
 Qy 803 acacaaaagaaatcctccatgtgaagctctctgtgaaagatttccaaagagatggcaa 862
 Db 659 ACACCAAAAGCGGCGGCGGCTGAGGCTGCTGCGAAGAACTTCCCAAGAGGAGGCCA 718
 Qy 863 cctaccttgatgtagcagcagcagctgagcttcttgaagaaacctgattatgagta 917
 Db 719 CGTACCTGCGCTATGTGCGGCGCTGGACTTCTTGAAGAGCCGACTATGACTA 773

RESULT 10
 W90174 466 bp mRNA linear EST 08-JUL-1996
 LOCUS zrh8b03.r1 Soares fetal_liver_spleen_JNPLS.S1 Homo sapiens cDNA
 DEFINITION clone IMAGE:418157 5' similar to SW:KCID_RAT 006486 CASEIN KINASE
 1, DELTA ISOFORM 1, mRNA sequence.
 ACCESSION W90174
 VERSION W90174.1 GI:1406473
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 466)
 AUTHORS Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
 'M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Maitra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,
 'R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project

Db	478	TGGCCAAAGAGTACATCGACCCCGGAGACCAAAAACACATCCCTACAGAGAGACACAGA	537
Qy	629	gtttaactcygaactcycaagatatatgtctatcaacaacgcatcttggcaaaagcgcaagcc	688
Db	538	GCTGTACACGGGGACGGCGCGGTACAGACATCCACACACCACCTCGGGAAGAAACAAAGCC	597
Qy	689	ggaagatgatttgtaagcccccgaagccatgatgtcatgtatctcttcgtgaagcaacccc	748
Db	588	GCAGGAGACACTGTGAACCGTTGGGCCATATGTTTATGTACTTCTCTCCGCGGAGACTTTC	657
Qy	749	cctggcaagagactcaagcgctgacacatataaagaagatataaaatgtgtgacacca	808
Db	658	CCTGGCAGAGGCGCTGAAGGCGGACACACACCAAGAGAGATGATAGAAATCGGGGACACACA	717
Qy	809	aaaggaatactcccatgaaagctctctgttgaagcttc	847
Db	718	AACGAGCCACGCGCGGTGAGAGTGCTGTGTGAGACTTTC	756
RESULT	12		
LOCUS	BG745206	868 bp	mRNA
DEFINITION	60272354Jpl NIH_MGC_113 Homo sapiens CDNA clone IMAGE:4849811 5',		linear EST 15-MAY-2001
ACCESSION	BG745206		
VERSION	BG745206.1	GI:14055859	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 868)		
AUTHORS	Mammalla; Eucheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://nigc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Dr. Mark Watson		
	CDNA Library Preparation: Ling Hong/Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		
	Plate: L16M1690 row: a column: 12		
	High quality sequence stop: 751.		
FEATURES			
SOURCE	location/Qualifiers		
	1..868		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4849811"		
	/clone_11b="NIH MGC 113"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: XhoI; EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene and Superscript II RT (Life Technologies)). Note: this is a NIH MGC Library."		
BASE COUNT	196 a	269 c	276 g
ORIGIN			127 t
Query Match	34.0%	Score 432;	DB 10;
Best Local Similarity	73.3%;	Pred. No. 2.2e-108;	Length 868;
Matches 608;	Conservative 0;	Mismatches 215;	Indels 7;
			Gaps 4;
Qy	89	gtctctcatcgtccctctggtgtcttattatgtgtggcccccaactcagggtgtgcaagaaga	148
Db	43	GCTTCGGGGACACAGCTTCGGGGGCTCGATGATGATGGGCCCAACTTCGCGCTGGCAAGAA	102

Accession	Source	Organism	Reference	Title	Journal	Comment
149	tagatg	ggaagactctgggaagagctcagatattgataatctcaacccaatgaaatc	208			
149	tagatg	ggaagactctgggaagagctcagatattgataatctcaacccaatgaaatc	208			
103	TCGGCTGGGGCAACTTCCGGGAGCTCCGCTTAGAAAGATATCTTATACAAATGAAATACG	162				
209	tagcatcaaacatggaacccaataaatacagctgctccacagcttcatttagaatcagat	268				
269	ttataaacagctctgcaagtcaggtggaatcctccacaggtgatacttacttgaccat	328				
223	TCCTACAAACAGCT---CAAGCGCCACAGAGGGGGCTCCCTCAGGCTTACATCTCGGCTCGT	279				
329	gtgggaatatatgatccatgctgtcggagagctcccttggccctcagctctggagaactgtctg	388				
280	GGGGAGACTACACCCCATGATGCTGAGAGCTCTGGGGCCCAAGCCTGGAGAGACCTGTTCG	339				
389	aacctctgtaccggaacattactcttgaagaagcgtgttaatgataagcatalccagctgtctt	448				
340	ACCTGTGGACCGGACCTTCAAGCTCAAGACCGGTCTGATGATCCCATCCAGCTGATCA	399				
449	ctcgaatgaaatagctgtcattcaagaacctatttaccagatgttaagccaggaact	508				
400	CGCGATGAGATATGTGACACACCAAGACCTTATACCGGAGCTGGAAGCCCGAAGCT	459				
509	tcctgatctgacgaagcaataagaagaagcagtgtatacacatatagaactcttgac	568				
460	TCCTGTGGGGCGCCGGGGACCAAGCGGAGCATGCCATCCATCATCATGACTTCGGGC	519				
559	tgagcaagaatatactgaccccggaacccaataaacacatactctatatagggaaacaaa	628				
520	TGGCCAAAGAGATCATCGACCCCGAGACCAAGAACATCCCTGATCCGCGAGCAACAGA	579				
629	gttaccctggaactctgcaagatatatgtctatcaaacagcattcttggcaagaagcaagcc	688				
560	GCCTACCGGGCGCGCGCTCATGAGCATTAACACGCACTGGGCAAGGAGCAGAGCC	639				
689	ggaagagatatttgaagagccctcagacatatgtcatgtatctcttggaggaagccttc	748				
640	-CGCGAGCAAGCTGAGGGGCTGGGCGCACATGTCATGACTTCTGGCGGCGACGATC	698				
749	cctggaagagctcaaggtctgacacattaaagaagaagatataaaaaaatgtgtgaccca	808				
699	CTGTGACAGGGGCTCAAGGGCGCACAGCTCAAGACGGGTACAGAAAGATCGGGGACACA	758				
809	aaagaataactccattgaagctctcttggaagacttcccaagaga-gatggcaacctac	867				
759	AACGGCCACGGGCTCGAGGTCTCTGAGAGAACTTCCAGAGGACGATGGACATGGTAC	818				
868	ctctgatatgtcagcgaactgagctcttggaaaaaacctgatatgagta 917					
819	CGGGCCCAAGT--GCGGGCTGACATCTTGGAGAGGCCGGAATACGACTA 866					


```

|||||
Db 252 GAATTAATCCATTGAAGTTCTCTGTGAAAACTCCAGAGAGATGCAACCTACTCGG 311
|||
Qy 873 atatgaagcgaactgactcttcttgaaaaaactgattatgaglatctacgacctctt 932
|||
Db 312 ATATGTCAGCGGATTAAGTCTTTGAAAAAAGCTGACTATGAGTATTTAGCGACGCTCT 371
|||
Qy 933 cacagacctcttgaagaaagagctacacaccttgactatgactatgattgggtggag 992
|||
Db 372 GACAGACCTCTTTGAAGGAAAGGCTACACCTTTGACTACNCGTATGATGGGTGGAG 431
|||
Qy 993 acctatccaccaccagtagtgcagt-tcacgtagatc-tggtagatcgaataact 1050
|||
Db 432 GCGTATGCGCCTCCATAGAGGTTAGTATGATGATGCTGATGCTGCTACTACT 491
|||
Qy 1051 cgaagaaagcacaacataagatcgccacacacagcactcttcgaatacagtg 1110
|||
Db 492 GGAGAAAGCCNCACACACAGGGGTGGNNCATGACACAGGCTTACGAATGAGGTG 551
|||
Qy 1111 g 1111
Db 552 g 552

RESULT 15
AA210141 466 bp mRNA linear EST 19-FEB-1997
LOCUS mu42901.r1 Soares_thymus_2NDBMT Mus musculus cDNA clone IMAGE:642096
DEFINITION 5' similar to TR:G854737 G854737 CASEIN KINASE 1 GAMMA 3 ISORFORM.
; mRNA sequence.
ACCESSION AA210141
VERSION AA210141.1 GI:1808459
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 466)
REFERENCE 1 (bases 1 to 466)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steppe,M., Tan,F., Underwood,R., Moore,B.,
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMT Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:394088
Seq primer: -28m13 rev2 ET from Amersham.
Location/Qualifiers
1. 466
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="642096"
/clone_id="Soares_thymus_2NDBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATGAGAGGAGCGCGCTTTTATTTTATTTTATTTTATTTTATTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

```

and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bernaldo."

```

BASE COUNT      138 a      109 c      103 g      116 t
ORIGIN
Query Match      32.6%; Score 413.4; DB 9; Length 466;
Best Local Similarity 94.2%; Pred. No. 2,4e-103;
Matches 440; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
|||
Qy 697 gatttgaagcccttaggcataatgattatcttcccttcgagcagccctccgagca 756
|||
Db 1 GATTGGAGACCTTTAGG-CATATGTTATATCTTCTCCGAGGACCTTACCTTGCGAA 59
|||
Qy 757 ggaactaagcgtgacacattaaagagagatcaaaaaatttggtagaccocaaaggaat 816
|||
Db 60 GGACTCAAGCCTGATACATTAATAAAGAGATATCAAAAAATCGGTATACCAAAAGGAAT 119
|||
Qy 817 accccattgaagctcctctgtgagaacttccagagagagatggaacctcctcgat 876
|||
Db 120 ACTCCATCGAAGCTCTGTGTGAGAACTTCCAGAGAGATGCGAACCTACCTTCGATAT 179
|||
Qy 877 gtaaggcactggaactcttgaaaaaactgattatgattatgacgacctctcaca 936
|||
Db 180 GTCAGGCGATTAGACTTCTTGAAAAACCTGATTATAGATTTTACGAGACCTTTTACA 239
|||
Qy 937 gacctcttgaagaaagagcctacacaccttgactatgactatgattgggtggagacct 996
|||
Db 240 GATCTGTTTACAGGAAAGGCTATACCTTGACTATGCTCTGATGATGGGTGGAAGGCT 299
|||
Qy 997 attcctactccagtagaggtcaagttcaagtagattcgttgatcttgcaataactcgaga 1056
|||
Db 300 ATTCTTACTCCAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
|||
Qy 1057 agccacacacatagagtagtcggccatcacacacagcagcctcttcgaataactgaagtttagc 1116
|||
Db 360 AGCCACACACACAGGAGTTCGGCCCTCACACACACAGCCTTTAATAATCAGTGTAGC 419
|||
Qy 1117 tcaaccatgagagctgaatgtagatgattccacagggagcccaact 1163
|||
Db 420 TCAACCAATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 466

```

Search completed: August 17, 2002, 20:54:15
Job time: 2169 sec
